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From: Whiteman, Brian
Sent: Friday, October 03, 2003 7:33 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

09/927,091 08/09/01 Killary et al.

search SEQ ID NO:1 against public databases.

search SEQ ID NO: 3 against public databases.

Thanks,
Brian Whiteman, 11e12
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
Crystal Mall 1, 11A16
(703) 305-0775

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

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AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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OM nucleic - nucleic search, using sw model

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(without alignments)
10494.448 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2252.8	58.9	30625	10	US-09-927-091-5
5	995.8	28.0	45845	10	US-09-927-091-6
6	838.6	21.9	49744	10	US-09-927-091-4
7	609.6	15.9	610	13	US-10-027-632-100265
8	562	14.7	573	9	US-09-864-761-7231
9	431	11.3	431	9	US-09-864-761-23962
10	136.4	3.6	1394	10	US-09-764-868-418
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ALIGNMENTS

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US-09-927-091-3	Sequence 3, Appli	
Patent No. US20020119541A1	GENERAL INFORMATION:	
APPLICANT: KILLARY, ANN	APPLICANT: CHANDLER, DAWN	
APPLICANT: LOTY, SREVE	FILE REFERENCE: UTSC:651US	
TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1	CURRENT APPLICATION NUMBER: US/09/927,091	
CURRENT FILING DATE: 2001-08-09	PRIOR APPLICATION NUMBER: 60/227,560	
PRIOR FILING DATE: 2000-08-23	PRIOR APPLICATION NUMBER: 60/225,033	
PRIOR FILING DATE: 2000-08-10	NUMBER OF SEQ ID NOS: 9	
SOFTWARE: Patentln Ver. 2.1	SEQ ID NO 3	
LENGTH: 3826	TYPE: DNA	
ORGANISM: Human	Query Match	100.0%; Score 3826; DB 10; Length 3826;
US-09-927-091-3	Best Local Similarity	100.0%; Pred. No. 0;
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DB	61	CCAGGCTTGGGGCCGGAATCCGAGCTGAGCGGGCCGCAACCCCTCTCTTCTTGGC 120
QY	121	GGTCACAGCAGCATGTACGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
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Sequence 7, Application US/09927091			
Patent No. US20020119541A1			
GENERAL INFORMATION:			
APPLICANT: KILLARY, ANN			
APPLICANT: LOFT, STEVE			
APPLICANT: CHANDLER, DAWN			
TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1			
FILE REFERENCE: US/SC:651US			
CURRENT APPLICATION NUMBER: US/09/927,091			
CURRENT FILING DATE: 2001-08-09			
PRIOR APPLICATION NUMBER: 60/227,560			
PRIOR FILING DATE: 2000-08-23			
PRIOR APPLICATION NUMBER: 60/225,033			
PRIOR FILING DATE: 2000-08-10			
NUMBER OF SEQ ID NOS: 9			
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OTHER INFORMATION: n - A or C or G or T/U			
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Mismatches 28; Indels 1; Gaps 1;			
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Dd	12480	GGTCCACAGCCTTCCCCCACTCAWCTCTCTCCCTCCCAACCCCAAGTCCAGCC	1253
Oy	1489	GCCTTAACCTTGAGACCGGGGACAGACCACAGCGCTGATCTGTGTGGAGACTGACCC	1548
Dd	12540	GCCCTTAACCCCTGGAGCCGGGGACAGCCACAGCGCTGATCTGTGTGGAGACTGACCC	1259
Oy	1549	ATTGAGGCTTACGGCACTTGCACCAACAGCAGCTGAGAGAGCTGCCAAGCGCTTGAT	1608
Dd	12600	ATTGTGGCTTACGGCACTTGCACCAACAGCAGCTGAGAGAGCTGCCAAGCGCTTGAT	1265
Oy	1609	GTGAGAGTGTGCGTCTGGGTTCTGAAGCCTTACAGTATGTGCGTCCACTGAGGAGTG	1668

Db	12660	GTGGAGGTTGTGCGTGGGTTCTGAAGACCTTACAGTATGTGGGCTCCACTACTGGGAGGTG	127139
QY	1669	GTGCTGGCGGAGAAAGACCCAGTGGGTGATCGGGCTGGCACACGAAGCCGCAAGCCGCAAG	1728
Db	12720	GTGCTGGCGGAGAAAGACCCAGTGGGTGATCGGGCTGGCACACGAAGCCGCAAGCCGCAAG	12779
QY	1729	GGCAGCAATCCAGATATCCAGGCCACCGCGGCTTCTACTGCATGCTGATGCAAGATGGCAAG	1788
Db	12780	GGCAGCAATCCAGATATCCAGGCCACCGCGGCTTCTACTGCATGCTGATGCAAGATGGCAAG	12839
QY	1789	CAGTACACAGCGCTGCACAGGAGCCCTGGACCGGCTTAAAGTCGCGGACAAAGCTTGACAG	1848
Db	12840	CAGTACAGCGCTGCACAGGAGCCCTGGACCGGCTTAAAGTCGCGGACAAAGCTTGACAG	12899
QY	1849	GTGGGTGTCTTTCCTGCACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGATGACATG	1908
Db	12900	GTGGGTGTCTTTCCTGCACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGATGACATG	12959
QY	1909	TTCCTGGCTTACACACTTCGCGGAGAAAGTTCCCTGGCAAGCTGTGCTTACTTCAAGCCT	1968
Db	12960	TTCCTGGCTTACACACTTCGCGGAGAAAGTTCCCTGGCAAGCTGTGCTTACTTCAAGCCT	13019
QY	1969	GGCCAGAGACCAACGCCAATGGCAGAAGAGTTCAACCGCTGGGATCAACACGTCGCGCATG	2028
Db	13020	GGCCAGAGACCAACGCCAATGGCAGAAGAGTTCAACCGCTGGGATCAACACGTCGCGCATG	13079
QY	2029	TAGTCCAGGAGAAAGAGACACACACTCTCTGGGACACTGCGACCTGCGAAGAGCCCTGC	2088
Db	13080	TAGTCCAGGAGAAAGAGACACACACTCTCTGGGACACTGCGACCTGCGAAGAGCCCTGC	13139
QY	2089	CCAGGAAGATATGAAAGAACTGGACTCCAGACCCACGTCGGCACTGGAGACCTCAAGGCCAGT	2148
Db	13140	CCAGG -AGATATGAAAGAACTGGACTCCAGACCCACGTCGGCACTGGAGACCTCAAGGCCAGT	13198
QY	2149	TGTTTACCCTTCAGACCCCTCCAGTCTGTATATAATGAGAGTTGCATTTCCCTACTTCTAAAGTC	2208
Db	13199	TGTTTACCCTTCAGACCCCTCCAGTCTGTATATAATGAGAGTTGCATTTCCCTACTTCTAAAGTC	13258
QY	2209	TCCTTCAGACATCGATGTCTGTAGCTCTGACCTTGATAGGAGATACAGCTTTGATCCAAAG	2268
Db	13259	TCCTTCAGACATCGATGTCTGTAGCTCTGACCTTGATAGGAGATACAGCTTTGATCCAAAG	13318
QY	2269	ATGTGACATAGGCTTCTCTCTCAAGGGCAACCCCTGCCCCAACCCCTCATCTCCCTCTCAAG	2328
Db	13319	ATGTGACATAGGCTTCTCTCTCAAGGGCAACCCCTGCCCCAACCCCTCATCTCCCTCTCAAG	13378
QY	2329	GGCAGGGGACTTACCTTCCAGTGTCTCTCCCTCCAGCCCGACGCCCTGACACTCGAGGAAGTGTGAG	2388
Db	13379	GGCAGGGGACTTACCTTCCAGTGTCTCTCCCTCCAGCCCGACGCCCTGACACTCGAGGAAGTGTGAG	13438
QY	2389	AGCATGGCCAGTATGTTGGCAGCCCGAAAGACACACAGACACCTTTATGTGCCATGGCCT	2448
Db	13439	AGCATGGCCAGTATGTTGGCAGCCCGAAAGACACACAGACACCTTTATGTGCCATGGCCT	13498
QY	2449	AAGACTTACCCCTGACCAAGCTATGTGATGGGCCATTACCCTTGGACCCAGTCCACAGTG	2508
Db	13499	AAGACTTACCCCTGACCAAGCTATGTGATGGGCCATTACCCTTGGACCCAGTCCACAGTG	13558
QY	2509	GTCACAGTATGATCTGTGCTGCTAGGGGTGGCAGAGGCCAACCTCTCCGCGCAACCCCAAC	2568
Db	13559	GTCACAGTATGATCTGTGCTGCTAGGGGTGGCAGAGGCCAACCTCTCCGCGCAACCCCAAC	13618
QY	2569	ACCAAGAACTATATGTGTTCTTACTTCTCCACACTGATCTCTGGTCAAGTATGATGCTGTG	2628
Db	13619	ACCAAGAACTATATGTGTTCTTACTTCTCCACACTGATCTCTGGTCAAGTATGATGCTGTG	13678
QY	2629	GCTGTGTGAAGGCACTGTGATTTGAGTCCACACATTTATAGCATGTGCGCACACCTTCC	2688
Db	13679	GCTGTGTGAAGGCACTGTGATTTGAGTCCACACATTTATAGCATGTGCGCACACCTTCC	13738
QY	2689	TGCCCCAAGGCCGAGGACAGGAGTGAGGAGATATCCAAAGCTGATGACAGGCCCATTTAGC	2748
Db	13739	TGCCCCAAGGCCGAGGACAGGAGTGAGGAGATATCCAAAGCTGATGACAGGCCCATTTAGC	13798

QY	2749	CTAAAGCACTGAGAGCAAGCCTCCCTGGATGATGAGAGTCCCAAGTACGCTGTGAA	2808
Db	13799	CTAAAGCAACTGGAGACAAGCCTCCCTGGATGATGAGAGTCCCAAGTACGCTGTGAA	13858
QY	2809	AGAGTCCAGCAACCCCTCTTCAGCAGAGCCTCTGTGACCTGCTAGGAGTGAAGAGCTTC	2868
Db	13859	AGAGTCCAGCAACCCCTCTTCAGCAGAGCCTCTGTGACCTGCTAGGAGTGAAGAGCTTC	13918
QY	2869	CAGAGCACTGTTGTTGTAATTAATTAAGACCCAGACACTGGAGGGGCTGTGGCTAGACCCCT	2928
Db	13919	CAGAGCACTGTTGTTGTAATTAATTAAGACCCAGACACTGGAGGGGCTGTGGCTAGACCCCT	13978
QY	2929	GTCAGACTGGCATCTATCTCAGTTAGATCTCGTCGACAGAAAACAAGAGCCACTGTG	2988
Db	13979	GTCAGACTGGCATCTATCTCAGTTAGATCTCGTCGACAGAAAACAAGAGCCACTGTG	14038
QY	2989	CTGGTTAATTAATTAACAAGATTACTACCTGGCCCTGTGTGCTTCAAAATTTGTGAA	3048
Db	14039	CTGGTTAATTAATTAACAAGATTACTACCTGGCCCTGTGTGCTTCAAAATTTGTGAA	14098
QY	3049	GAGCTGGAGAAAGCAGACTCTGCTGAATTTCCAGAACTCCACAGCCCAATTCATCTATCT	3108
Db	14099	GAGCTGGAGAAAGCAGACTCTGCTGAATTTCCAGAACTCCACAGCCCAATTCATCTATCT	14158
QY	3109	CTGTTGTGACAGAGAAAGCTGCCCCATCTGACAGAAAGCAGCATCTCCAGAAAGCTGCTG	3168
Db	14159	CTGTTGTGACAGAGAAAGCTGCCCCATCTGACAGAAAGCAGCATCTCCAGAAAGCTGCTG	14218
QY	3169	ACTGACAGAACTAGGCTCCCTCTGTGCACAGGTCCTGCCAGCAATAGATGCTCTAGGCT	3228
Db	14219	ACTGACAGAACTAGGCTCCCTCTGTGCACAGGTCCTGCCAGCAATAGATGCTCTAGGCT	14278
QY	3229	GCCTCTCCCTCACTCACTCAGTCCCAATCTAAATTTTACAAAGATTCGTTGGG	3288
Db	14279	GCCTCTCCCTCACTCACTCAGTCCCAATCTAAATTTTACAAAGATTCGTTGGG	14338
QY	3289	GGAACCTTAAGTCAGATCCAGAACCTTGGCTGCAGAGGAGTCTGGAAATGTCAATTTCCCT	3348
Db	14339	GGAACCTTAAGTCAGATCCAGAACCTTGGCTGCAGAGGAGTCTGGAAATGTCAATTTCCCT	14398
QY	3349	AGAAAGAAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTTTCGCCAAGCAATCCAA	3408
Db	14399	AGAAAGAAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTTTCGCCAAGCAATCCAA	14458
QY	3409	TCGTGAAGAACTCGGAGAGGGGTGAGTCCACATCTAGGGTTGCTCGCCCTTGACTCT	3468
Db	14459	TCGTGAAGAACTCGGAGAGGGGTGAGTCCACATCTAGGGTTGCTCGCCCTTGACTCT	14518
QY	3469	ATCCCTCCCGCAGAGTGGGAACCTGAGAGATGGGCGCAAACTGAGCCTAAATGTCTCC	3528
Db	14519	ATCCCTCCCGCAGAGTGGGAACCTGAGAGATGGGCGCAAACTGAGCCTAAATGTCTCC	14578
QY	3529	CCGGCCTTGAATTTCTTTCTAGTCCCTGGGGCCTAGATTCTGCACTTGGGGCTCTGACA	3588
Db	14579	CCGGCCTTGAATTTCTTTCTAGTCCCTGGGGCCTAGATTCTGCACTTGGGGCTCTGACA	14638
QY	3589	CAACACACATCCCAAAAGTACCGGAAAGACTTAAACACAGGGGTTCTTAAATGGCTCC	3648
Db	14639	CAACACACATCCCAAAAGTACCGGAAAGACTTAAACACAGGGGTTCTTAAATGGCTCC	14698
QY	3649	CCCCGCCACCCGGGCTCTCTTGGGCAAAAAGAAATGTACAGCCTACCCCAACCTTCAA	3708
Db	14699	CCCCGCCACCCGGGCTCTCTTGGGCAAAAAGAAATGTACAGCCTACCCCAACCTTCAA	14758
QY	3709	CTACACAAATCTGGGCCACCCACAGCAATATTTATTTAAATGTGTGCCATTTATGAG	3768
Db	14759	CTACACAAATCTGGGCCACCCACAGCAATATTTATTTAAATGTGTGCCATTTATGAG	14818
QY	3769	TTATGATCAATTTGTATTAATTAAGTTACAGATGTCA	3807
Db	14819	TTATGATCAATTTGTATTAATTAAGTTACAGATGTCA	14857

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RESULT 3
US-09-927-091-8
; Sequence 8, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTY, STEVE
; APPLICANT: CHANDLER, DAMN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: US/651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentlin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30676
; TYPE: DNA
; ORGANISM: Human
; NAME/REV: modified_base
; LOCATION: (6671)..(30676)
; OTHER INFORMATION: n = A or C or G or T/U
US-09-927-091-8

Query Match      60.3%; Score 2308.6; DB 10; Length 30676;
Matches 2387; Conservatively 98.7%; Pred. No. 0;
Matches 2387; Mismatches 0; Indels 29; Gaps 2;

1429 GGCCTTACCTGAGTACATCATCTGAGAGTCCCTGTTCCAGAGATCCACCCAGTCCAGGC 1488
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23371 GGTCCACACCTTCTTCCACATCATCTTCTTCTTCCCTCCACACCCACAGTCCAGCC 23430
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1489 GCCCTTAACTGAGACCCGAGACAGCCACAGCCAGCTGATCTGTGAGAGACTGACAC 1548
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 22431 GCCCTTAACTGAGACCCGAGACAGCCACAGCCAGCTGATCTGTGAGAGACTGACAC 22490
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1549 ATTGAGCTTACGAGCAATCTGACACAGCCACCTGACAGACTGCGCAAGAGCCCTCGAT 1608
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23491 ATTGAGCTTACGAGCAATCTGACACAGCCACCTGACAGACTGCGCAAGAGCCCTCGAT 23550
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1609 GTGAGAGTCTCGGTGCTGAGTCTGAGAGCTTCAAGCTTCAAGTGCCTCCACTACTGGAGTG 1668
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23551 GTGAGAGTCTCGGTGCTGAGTCTGAGAGCTTCAAGCTTCAAGTGCCTCCACTACTGGAGTG 23610
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1669 GTGAGTGGGAGAGAACCAAGTGGGTGATCGGGCTGGACACAGAGCCGCAAGCCGCAAG 1728
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 22611 GTGAGTGGGAGAGAACCAAGTGGGTGATCGGGCTGGACACAGAGCCGCAAGCCGCAAG 22669
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1729 GGCAGATCCAGATCCAGAGCCAGCCGCGCTTCTACTGATCTGATGACAGATGGCAAC 1788
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23670 GGCAGATCCAGATCCAGAGCCAGCCGCGCTTCTACTGATCTGATGACAGATGGCAAC 23729
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1789 CAGTACAGGCTGACAGAGCCCTGAGAGCGGCTTAAGCTCCGGAGCAAGTGTGAAG 1848
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23730 CAGTACAGGCTGACAGAGCCCTGAGAGCGGCTTAAGCTCCGGAGCAAGTGTGAAG 23789
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1849 GTGGGTGTCTTCTGAGTATGACAAAGCTTGCTATCTTCAATGCTGATGACATG 1908
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23790 GTGGGTGTCTTCTGAGTATGACAAAGCTTGCTATCTTCAATGCTGATGACATG 23849
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1909 TCTTGGCTTACACCTTCCGAGAGATCCCTGGGCAACTCTGCTCTTACTTACACCT 1968
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23850 TCTTGGCTTACACCTTCCGAGAGATCCCTGGGCAACTCTGCTCTTACTTACACCT 23909
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

1969 GGCACAGGCTGAGCAATGGCAAGAGTTCAGAGCCCTGCGGATCAACACCGTCCGATC 2028
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23910 GGCACAGGCTGAGCAATGGCAAGAGTTCAGAGCCCTGCGGATCAACACCGTCCGATC 23969
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```
2029 TAGTCCAGGACAGAGAGACACACACTCTCTGGGACCACTGCGACCTGCAAGAGCCCTGC 2088
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 23970 TAGTCCAGGACAGAGAGACACACACTCTCTGGGACCACTGCGACCTGCAAGAGCCCTGC 24029
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2089 CCAGAGAGATAGAGAGCTGAGACTCCAGCCACACCGTGGCCACTGAGAGACTCAGGCCACT 2148
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24030 CCAGG-AGATAGAGAGCTGAGACTCCAGCCACACCGTGGCCACTGAGAGACTCAGGCCACT 24088
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2149 TGTTTACCTCCAGCTCCAGCTGCTGTAATGAGAGTTCATCTCTACTTCTTAACCTC 2208
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24089 TGTTTACCTCCAGCTCCAGCTGCTGTAATGAGAGTTCATCTCTACTTCTTAACCTC 24148
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2209 TCTTCCAGCATGATCTGTGATGCTGACCTTGTATAGGATATACGCTTGTATCCAAAG 2268
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24149 TCTTCCAGCATGATCTGTGATGCTGACCTTGTATAGGATATACGCTTGTATCCAAAG 24208
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2269 ATGTGACATGCTTCTCCAGAGGCAACCCCTGCCAACCCCTATCCCATCTTCTCAG 2328
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24209 ATGTGACATGCTTCTCCAGAGGCAACCCCTGCCAACCCCTATCCCATCTTCTCAG 24268
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2329 GGCAGGGACTACCTTCCAGTGTCTCTCCAGCCAGCCCTGACCTCAGAGAGTGTCAAG 2388
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24269 GGCAGGGACTACCTTCCAGTGTCTCTCCAGCCAGCCCTGACCTCAGAGAGTGTCAAG 24328
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2389 AGCATGGCAGTATGTTGGACGCCGAAAGACACAGACACCTTATGTCCATGAGCT 2448
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24329 AGCATGGCAGTATGTTGGACGCCGAAAGACACAGACACCTTATGTCCATGAGCT 24388
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2449 AAGACTTACCCCTGACCAAGCTGATGAGGCCATTTACCTTGACCCTGACCTACAGTG 2508
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24389 AAGACTTACCCCTGACCAAGCTGATGAGGCCATTTACCTTGACCCTGACCTACAGTG 24448
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2509 GTACAGATGATGATCTGCTGATGCTGAGAGGCCAACTCTCCAGCCAGCCAGCCAG 2568
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24449 GTACAGATGATGATCTGCTGATGCTGAGAGGCCAACTCTCCAGCCAGCCAGCCAG 24508
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2569 ACCAAGACTATATGTTCTCTACTTCTCCACTGATCTGCTGATGATGATGATGCTGTG 2628
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24509 ACCAAGACTATATGTTCTCTACTTCTCCACTGATCTGCTGATGATGATGATGCTGTG 24568
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2629 GCCTGTGGAAGGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2688
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24569 GCCTGTGGAAGGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 24628
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2689 TGCCCAAGGCGGAGGAGACAGGGTGAAGGATATCCCAAGCTGATCAGAGCCCATTAAG 2748
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24629 TGCCCAAGGCGGAGGAGACAGGGTGAAGGATATCCCAAGCTGATCAGAGCCCATTAAG 24688
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2749 CTAAAAAGCACTGACAGACAGCCCTCTGATGATGATGATGATGATGATGATGATGATG 2808
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24689 CTAAAAAGCACTGACAGACAGCCCTCTGATGATGATGATGATGATGATGATGATGATG 24748
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2809 AGAGTCCAGCAACCTCTTCCAGCCAGCCCTCTGATGATGATGATGATGATGATGATGATG 2868
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24809 AGAGTCCAGCAACCTCTTCCAGCCAGCCCTCTGATGATGATGATGATGATGATGATGATG 24868
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2869 CAGAACAGTGTGTATATAGAGACCAAGCACTGAGAGGGGCTGTGGTAGACCCCTT 2928
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24809 CAGAACAGTGTGTATATAGAGACCAAGCACTGAGAGGGGCTGTGGTAGACCCCTT 24868
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2929 GTCAGACTTGGCATCTATCTCACTAGATCTGCTGACAGAAAAAAGAGCCACTGTAG 2988
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24869 GTCAGACTTGGCATCTATCTCACTAGATCTGCTGACAGAAAAAAGAGCCACTGTAG 24928
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

2989 CTGGTTAATATACAAAGATTTACTATCTGAGGCGCTGAGGCTTGCAGAAATTTGTGAA 3048
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24929 CTGGTTAATATACAAAGATTTACTATCTGAGGCGCTGAGGCTTGCAGAAATTTGTGAA 24988
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

3049 GAGCTGAGAGAGAGACTCTGCTGAATTTCCAGAGAACTCCACAGCCAGATTCATCATG 3108
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24989 GAGCTGAGAGAGAGACTCTGCTGAATTTCCAGAGAACTCCACAGCCAGATTCATCATG 25048
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

3109 CTGTGTGACAGAGAAAGCTGCCCATCTGTGAGAGAGCACTATGCCAGAAAAGCTGTG 3168
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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Db	25049	CTGTGTGGACACAGAAAGCGTCCCATCTGCAGGAAAGCCACTATGCCAGAAAGCTGCTG	25108
QY	3169	ACTGCACAACTAGAGCTCCCTCTGCGACGGGTCCGTGCACCAATAGATCTCTGAGGCGCT	3228
Db	25109	ACTGCAGAACTAGGCTTCCTCTCTGCCAGGTCCTGTCAGCCAAATATCTCTCGAGGCTT	25168
QY	3229	GCCCCCTCTCCCACTTCACCTAGTTCGCAAACTCTAAATTTTACAGAGATTTGTTTGGG	3288
Db	25169	GCCCCCTCTCCCACTTCACCTAGTTCGCAAACTCTAAATTTTACAGAGATTTCTGTTTGGG	25228
QY	3289	GGAACCTTAAGTCAGATCCAGAACCTTGGCGCAAGGAGATCTGCGGAAATAGCTATTTCCCT	3348
Db	25229	GGAACCTTAAGTCAGATCCAGAACCTTGGCGCAAGGAGATCTGCGGAAATAGTATTTCCCT	25288
QY	3349	AGAAAGAAAGTTAGAGGTGGGTGGTGGAGCAAGCCCCACCTGCTTTTCTGCCACAGCATCCAA	3408
Db	25289	AGAAAGAAAGTTAGAGGTGGGTGGTGGAGCAAGCCCCACCTGCTTTTCTGCCACAGCATCCAA	25348
QY	3409	TCTGTGAAGAACTCTGGGAGAGAGGTGTGACATCTTAGGGTTGTCTGCCCCCTTGCTCT	3468
Db	25349	TCTGTGAAGAACTCTGGGAGAGAGGTGTGACATCTTAGGGTTGTCTGCCCCCTTGCTCT	25408
QY	3469	ATCCCTTCGCCAGAGAGTGGGAACCTGAGAGAGTGGGCGCAAGACTGAGCCTTAATGTCTCC	3528
Db	25409	ATCCCTTCGCCAGAGAGTGGGAACCTGAGAGAGTGGGCGCAAGACTGAGCCTTAATGTCTCC	25468
QY	3529	CCGGCCCTTGACTTTTCTCTCTCTAGTCTCTGGGCCCTAGATTTCTGCATTTGGGGTCTTGACA	3588
Db	25469	CCGGCCCTTGACTTTTCTCTCTCTAGTCTCTGGGCCCTAGATTTCTGCATTTGGGGTCTTGACA	25528
QY	3589	CAACACACACATCTCCCAAAAGTATGCGGGAAGATCTAAACAGAGGGGGTCTTAAATGGCTCC	3648
Db	25529	CAACACACACATCTCCCAAAAGTATGCGGGAAGATCTAAACAGAGGGGGTCTTAAATGGCTCC	25588
QY	3649	CCCCGCCACCCGGGGCCTCCCTTGGGCAAAAAGAAATTTGTCAGGCTTACCCCAACCCCTTCAA	3708
Db	25589	CCCCGCCACCCGGGGCCTCCCTTGGGCAAAAAGAAATTTGTCAGGCTTACCCCAACCCCTTCAA	25648
QY	3709	CTACAGAAATCTGGGGCACCCACGACGATTTTTTATTATTAATTTGGCCATTTTATGAG	3768
Db	25649	CTACAGAAATCTGGGGCACCCACGACGATTTTTTATTATTAATTTGGCCATTTTATGAG	25708
QY	3769	TTATGATCAATTTGTATTAAATTTAAAGTTTACAGATGTCA	3807
Db	25709	TTATGATCAATTTGTATTAAATTTAAAGTTTACAGATGTCA	25747
RESULT 4			
US-09-927-091-5			
: Sequence 5, Application US/09927091			
: Patent No. US20020119541A1			
: GENERAL INFORMATION:			
: APPLICANT: KITILARY, ANN			
: APPLICANT: LOTT, STEVE			
: APPLICANT: CHANDLER, DAMN			
: TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1			
: FILE REFERENCE: UTSC:651US			
: CURRENT APPLICATION NUMBER: US/09/927,091			
: PRIOR FILING DATE: 2001-08-09			
: PRIOR APPLICATION NUMBER: 60/327,560			
: PRIOR FILING DATE: 2000-08-23			
: PRIOR APPLICATION NUMBER: 60/225,033			
: PRIOR FILING DATE: 2000-08-10			
: NUMBER OF SEQ ID NOS: 9			
: SOFTWARE: PatentIn Ver. 2.1			
: SEQ ID NO 5			
: LENGTH: 30625			
: TYPE: DNA			
: ORGANISM: Human			
: FEATURE:			
: NAME/KEY: modified_base			
: LOCATION: (4754)..(30625)			

! OTHER INFORMATION: n - A or C or G or T/U
US-09-927-091-5

Query Match	58.9%	Score 2252.8;	DB 10;	Length 30625;
Best Local Similarity	97.5%;	Pred. No. 0;		
Matches 2320;	Conservative 0;	Mismatches 57;	Indels 3;	Gaps 3;

QY	1429	GGCCCCCTCAGACACACATCTGGAAAGTCCCGTCTCCAGAGACATCCACCCAGTGCAGGC	1488
Db	21906	GGTCCACACCCCTTCTCCCACTCATCTCTCTCTCCCTCTCCAAACCCCAAGTCCAGCC	21965
QY	1489	GGCCTTAACCTTGAACCCGGGGCACAGCCCAACAGGCGCTGATCTGTCTGGAGACTGCACC	1548
Db	21966	GGCCTTAACCTTGAACCCGGGGCACAGCCCAACAGGCGCTGATCTGTCTGGAGACTGCACC	22025
QY	1549	ATTGTGGCTTAAAGGCAACTTGCACCCACAGCACTGCAGAGCTCGGCCAAAGCGCTTGAT	1608
Db	22026	ATTGTGGCTTAAAGGCAACTTGCACCCACAGCACTGCAGAGCTCGGCCAAAGCGCTTGAT	22085
QY	1609	GTGGAGGTGTCCGGTCTGGGTTCTGAAGCCTTTCAGTACTGGCTGCACACTACTGGAGGTG	1668
Db	22086	GTGGAGGTGTCCGGTCTGGGTTCTGAAGCCTTTCAGTACTGGCTGCACACTACTGGAGGTG	22145
QY	1669	GTGGTGGCGGAAGAAAGCCAGTGGGTGATTCGGGCTGGACACAGAAAGCCGAAGCCGAAG	1728
Db	22146	GTGGTGGCGGAAGAAAGCCAGTGGGTGATTCGGGCTGGACACAGAAAGCCGAAGCCGAAG	22205
QY	1729	GGCAGCATCCAGTCCAGGCGCGCGGCTTCTACTGCATCTGATGTACAGATGGCAAC	1788
Db	22206	GGCAGCATCCAGTCCAGGCGCGCGGCTTCTACTGCATCTGATGTACAGATGGCAAC	22265
QY	1789	CATTAAAGGGCCTGCACGGAGGCCCTTGGACGGGGCTTAACGTCCGGGACAAGCTTGAACAG	1848
Db	22266	CATTAAAGGGCCTGCACGGAGGCCCTTGGACGGGGCTTAACGTCCGGGACAAGCTTGAACAG	22325
QY	1849	GTGGGTGTCTTCTGTGACTATACCAAGGCTTGCATCTTCTACATAGCTGATGACATG	1908
Db	22326	GTGGGTGTCTTCTGTGACTATACCAAGGCTTGCATCTTCTACATAGCTGATGACATG	22385
QY	1909	TCTTGACTCTAACACTTCCGGGAAAGTTCCCTGGCAAGCTCTGCTCTTACCTTCAGCCCT	1968
Db	22386	TCTTGACTCTAACACTTCCGGGAAAGTTCCCTGGCAAGCTCTGCTCTTACCTTCAGCCCT	22445
QY	1969	GGCACAAGCAGCGCAATGGCAAGAACGTTCAGGCGCTGGCGATCAACACGTCGGCATC	2028
Db	22446	GGCACAAGCAGCGCAATGGCAAGAACGTTCAGGCGCTGGCGATCAACACGTCGGCATC	22505
QY	2029	TAGTCCAGGCGAAGAGACACAAACCTCTGGGACCACTGCCACCTGCAGAAGCCCTGC	2088
Db	22506	TAGTCCAGGCGAAGAGACACAAACCTCTGGGACCACTGCCACCTGCAGAAGCCCTGC	22564
QY	2089	CCAGGAAGATTAANAACCTCGAATCTCAGACCCACCGTGGCCACTGAGAACTCAGGCGAGT	2148
Db	22565	CCAGG-AGATTAANAACCTCGAATCTCAGACCCACCGTGGCCACTGAGAACTCAGGCGACT	22623
QY	2149	TGTTTACCCCTCAGAGCTCCAGTCTGTAAATAGAGAGTTGCATTCCTACATTCCAAACTC	2208
Db	22624	TGTTTACCCCTCAGAGCTCCAGTCTGTAAATAGAGAGTTGCATTCCTACATTCCAAACTC	22683
QY	2209	TCTTCCAGCATGATGTTCTGTAGCTTGACCTTGATAGGATACAGCTTGTGATCCAAG	2268
Db	22684	TCTTCCAGCATGATGTTCTGTAGCTTGACCTTGATAGGATACAGCTTGTGATCCAAG	22743
QY	2269	ATGTGACATGGGTTTCTTCCAGGGGAACCCCTGCCAAACCTCTATCCCATCTTTCAGG	2328
Db	22744	ATGTGACATGGGTTTCTTCCAGGGGAACCCCTGCCAAACCTCTATCCCATCTTTCAGG	22803
QY	2329	GGCAGGGGACTACTTCCAGTGTCTCCCTCCAGGCCCAAGCCCTGCACAGAGAGTGTCAAG	2388
Db	22804	GGCAGGGGACTACTTCCAGTGTCTCCCTCCAGGCCCAAGCCCTGCACAGAGAGTGTCAAG	22863
QY	2389	AGCATGGCAGTATGTTGGCAGCCGGAAGACACACAGACCCCTTATGTCTCCATGGCCT	2448

Db 22864 AGCATGGCCAGTAGTGGCAGGCCGAAAGACACAGCACCCTTATGTGCCATGGCCT 22923
 Oy 2449 AAGATTACCCCTGCAACAGCTAGTAGAGGCCATTACCCCTTGAGCCCAAGTCCACAGTG 2508
 Db 22924 AAGACTTACCCCTGCAACAGCTAGTAGAGGCCATTACCCCTTGAGCCCAAGTCCACAGTG 22983
 Oy 2509 GTCAACAGTACCTGCTGCTAGAGGTTGCTGAGAGCCACACTCTCTGCGCACCCCCAC 2568
 Db 22994 GTCAACAGTACCTGCTGCTAGAGGTTGCTGAGAGCCACACTCTCTGCGCACCCCCAC 23043
 Oy 2569 ACCAAGACTATATGTTCT 2628
 Db 23044 ACCAAGAAATATATGTTCT 23103
 Oy 2629 GCTGTGGAAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2688
 Db 23104 GCTGTGGAAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 23163
 Oy 2689 TGCCCAAGGCGGAGGAGCAGGGGTAGGGTATACCCAAAGCTGATGACAGGCCATTAGC 2748
 Db 23164 TGCCCAAGGCGGAGGAGCAGGGGTAGGGTATACCCAAAGCTGATGACAGGCCATTAGC 23223
 Oy 2749 CTAAAGCACTGCGAGCAACGCTCCCTGATGATGAGTGCAGGTCAGAGCTGAGACA 2808
 Db 23224 CTAAAGCACTGCGAGCAACGCTCCCTGATGATGAGTGCAGGTCAGAGCTGAGACA 23283
 Oy 2809 AGAGTCAGCAACCCCTCTTACGACGAGGCTCTGACCTGCTAGAGGTGACAGAGGCTTC 2868
 Db 23284 AGAGTCAGCAACCCCTCTTACGACGAGGCTCTGACCTGCTAGAGGTGACAGAGGCTTC 23343
 Oy 2869 CAGAAAGCTGTTTATATAGGACCCAGCACT- GGGAGGGGCTGTTGGCTAGACCCCT 2927
 Db 23344 CAGAAAGCTGTTTATATAGGACCCAGCACTGGGGGGGCTGTTGGCTAGAAACCCCT 23403
 Oy 2928 TGTGACACTTGGCATCTATCTCAGTTAGGATCTGCTGAGAGAAACAGAGCCACTGTGA 2987
 Db 23404 TGTGACACTTGGCATCTATCTCAGTTAGGATCTGCTGAGAGAAACAGAGCCACTGTGA 23463
 Oy 2988 GCTGTTTAAATTAGCAAGGATTTACTACCTGGCCCTGGTGGCTGCAAAATTTGTGGA 3047
 Db 23464 GCTGTTTAAATTAGCAAGGATTTACTACCTGGCCCTGGTGGCTGCAAAATTTGTGGA 23523
 Oy 3048 AGAGCTGAGAGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3107
 Db 23524 AGAGCTGAGAGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 23583
 Oy 3108 TCTGTTGACGAGGAAAGCTCCGCCCATCTGACAGAGGACCTATGCGAGAAAGCTGCT 3167
 Db 23584 TCTGTTGACGAGGAAAGCTCCGCCCATCTGACAGAGGACCTATGCGAGAAAGCTGCT 23643
 Oy 3168 GACTGACAGACTAGGCTCCCTCTGCGACGCTCCGTCGCGCAAGCAATGATGCTGAGGCC 3227
 Db 23644 GACTGACAGACTAGGCTCCCTCTGCGACGCTCCGTCGCGCAAGCAATGATGCTGAGGCC 23703
 Oy 3228 TGCCCTCTCCACTTCACTCAGTTCCAAATCTAAATTTTACAGAGATTTCTGTTGG 3287
 Db 23704 TGCCCTCTCCACTTCACTCAGTTCCAAATCTAAATTTTACAGAGATTTCTGTTGG 23763
 Oy 3288 GGGAACTTAAAGTCAATCCAGAACTTGGCTGACAGGAGTGTGGAAATGCTATTTGCC 3347
 Db 23764 GGGAACTTAAAGTCAATCCAGAACTTGGCTGACAGGAGTGTGGAAATGCTATTTGCC 23833
 Oy 3348 TAGAAGAGTATAGGTGGGTGAGCAAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3407
 Db 23824 TAGAAGAGTATAGGTGGGTGAGCAAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 23883
 Oy 3408 ATCTGAAAGAACTGGGAGAGGGTGGAGTCCATCTAGAGTGTGCTGCTGCTGCTGCTGCTGCT 3467
 Db 23884 ATCTGAAAGAACTGGGAGAGGGTGGAGTCCATCTAGAGTGTGCTGCTGCTGCTGCTGCTGCT 23943
 Oy 3468 TATCCCTGCGCAGAGTGGGAAGTGGAGAGTGGGCTGCAACATGAGAGCTTAAATGCTC 3527
 Db 23944 TATCCCTGCGCAGAGTGGGAAGTGGAGAGTGGGCTGCAACATGAGAGCTTAAATGCTC 24003

Oy 3528 CCCGCGCTTGACTTTTCTTTCTAGTCCGCGGCTAGATTCTGCACTTGGGCTCTGTGAC 3587
 Db 24004 CCCGCGCTTGACTTTTCTTTCTAGTCCGCGGCTAGATTCTGCACTTGGGCTCTGTGAC 24063
 Oy 3588 ACACACACATCCCAAGATAGCCGGAAGACTTAAACACAGGGGCTTCTTAAATGCTG 3647
 Db 24064 ACACACACATCCCAAGATAGCCGGAAGACTTAAACACAGGGGCTTCTTAAATGCTG 24123
 Oy 3648 CCCCGCGCAGCGGCGCTCCCTGGGCAAAAGAAATGTCAGACCCCTACCCCAACCTTCA 3707
 Db 24124 CCCCGCGCAGCGGCGCTCCCTGGGCAAAAGAAATGTCAGACCCCTACCCCAACCTTCA 24183
 Oy 3708 ACTACAGATCTGGGCGCACCCAGCAGTATTTTATTTAAATGTTGCCATTTTATGA 3767
 Db 24184 ACTACAGATCTGGGCGCACCCAGCAGTATTTTATTTAAATGTTGCCATTTTATGA 24243
 Oy 3768 GTTATGATCAATTTTATTTAAATTTAAAGTTACAGATGCA 3807
 Db 24244 GTTATGATCAATTTTATTTAAATTTAAAGTTACAGATGCA 24283

RESULT 5

US-09-927-091-6
 ; Sequence 6, Application US/09927091
 ; Patent No. US20020119541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KILARY, ANN
 ; APPLICANT: LOTT, STEVE
 ; APPLICANT: CHANDLER, DAMN
 ; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
 ; FILE REFERENCE: UTSC:651US
 ; CURRENT APPLICATION NUMBER: US/09/927,091
 ; CURRENT FILING DATE: 2001-08-09
 ; PRIOR FILING DATE: 60/227,560
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: 60/225,033
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 45845
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-927-091-6

Query Match 26.0%; Score 995.8; DB 10; Length 45845;
 Best Local Similarity 99.7%; Pred. No. 2.5e-263;
 Matches 1008; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 1 AGCTGCGCTGAGACCGAAGCGGTGCTGCTAGCTCGCGGGGTAAAGGGTGCAGCTGGG 60
 Db 24164 AGCTGCGCTGAGACCGAAGCGGTGCTGCTAGCTCGCGGGGTAAAGGGTGCAGCTGGG 24223
 Oy 61 CCAGGGTTTGGGGCCGGGATCCGCAAGCTGAGCGGGCCCGGACCCCTCTCTCTGCGC 120
 Db 24224 CCAGGGTTTGGGGCCGGGATCCGCAAGCTGAGCGGGCCCGGACCCCTCTCTCTGCGC 24283
 Oy 121 GGTACAGCAATGTACGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 Db 24284 GGTACAGCAATGTACGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 24343
 Oy 181 GCTTTCGCGCTCCCGCGACGCGCCGACCCGAGGATTTGACGCCCTTAAAGGGTCCAC 240
 Db 24344 GCTTTCGCGCTCCCGCGACGCGCCGACCCGAGGATTTGACGCCCTTAAAGGGTCCAC 24403
 Oy 241 CCCGCTCGGGATTCCTTCTTCTCCAGTCTCTATCCCTTAAAGTGGCTGCTGCTGCTGCT 300
 Db 24404 CCCGCTCGGGATTCCTTCTTCTCCAGTCTCTATCCCTTAAAGTGGCTGCTGCTGCTGCT 24463
 Oy 301 CCTCCCGCTCAGAGTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Db 24464 CCTCCCGCTCAGAGTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 24523

QY 361 TTGAGCTGCCACTACCTTAGACTGCCCTCCGGGCTGGCTCCAGGAGTCTACGC 420
| | | | |
Db 24524 TTGAGCTGCCACTACCTTAGACTGCCCTCCGGGCTGGCTCCAGGAGTCTACGC 24583
| | | | |
QY 421 GCGAGCCCTTCTCCGGGTTACCTCTCTCCGAGACAGACCCCTCTCTCCGGTACG 480
| | | | |
Db 24584 GCGAGCCCTTCTCCGGGTTACCTCTCTCCGAGACAGACCCCTCTCTCCGGTACG 24643
| | | | |
QY 481 TCCATACCTTCTCCGGGCTCTGTCGCCGAGCCCTGCGGTCTGCTCCGACA 540
| | | | |
Db 24644 TCCATACCTTCTCCGGGCTCTGTCGCCGAGCCCTGCGGTCTGCTCCGACA 24703
| | | | |
QY 541 GCGCGGCTCTCTACGCCGCCCTTCCCTTCCGGGCTCTCTGCTGCCCTGCG 600
| | | | |
Db 24704 GCGCGGCTCTCTACGCCGCCCTTCCCTTCCGGGCTCTCTGCTGCCCTGCG 24762
| | | | |
QY 601 GCCATGCGCTGACACCTTCAAGAGAGAGAGTCTGTGCTCCATCTCTCCGAGATCTACAG 660
| | | | |
Db 24763 GCCATGCGCTGACACCTTCAAGAGAGAGAGTCTGTGCTCCATCTCTCCGAGATCTACAG 24822
| | | | |
QY 661 GACCCGCTGAGACCTGCGGCTCGAGACACTTCTGCGCGCTGATCAGGAGACAGTGG 720
| | | | |
Db 24823 GACCCGCTGAGACCTGCGGCTCGAGACACTTCTGCGCGCTGATCAGGAGACAGTGG 24882
| | | | |
QY 721 GTGCGGACGAGAGCGGAGCGGCGCGGAGCTGCCGAGTGGCGGCGACGTTTGGCGAG 780
| | | | |
Db 24883 GTGCGGACGAGAGCGGAGCGGCGCGGAGCTGCCGAGTGGCGGCGACGTTTGGCGAG 24942
| | | | |
QY 781 CCGCGGCTGGGCGCCACCTTCAAGCTGGCCAACTGCTGGAGCGCTACAGTCTTCCCG 840
| | | | |
Db 24943 CCGCGGCTGGGCGCCACCTTCAAGCTGGCCAACTGCTGGAGCGCTACAGTCTTCCCG 25002
| | | | |
QY 841 CTGAGACGCACTCTCAAGCGGCGCGCGCGGAGCCTGCGAGCGGAGCAAGCAAGTTC 900
| | | | |
Db 25003 CTGAGACGCACTCTCAAGCGGCGCGCGGAGCCTGCGAGCGGAGCAAGCAAGTTC 25062
| | | | |
QY 901 AAGCTCTTCTGCTCTACAGGAGCGGCGCTTCTGCTTCTTCTGAGAGAGCTGCACTG 960
| | | | |
Db 25063 AAGCTCTTCTGCTCTACAGGAGCGGCGCTTCTGCTTCTTCTGAGAGAGCTGCACTG 25122
| | | | |
QY 961 CACGAGCAGATCAGTCAACCGGATGAGAGAGCGCTTGCAGCGAGCTGCGAG 1011
| | | | |
Db 25123 CACGAGCAGATCAGTCAACCGGATGAGAGAGCGCTTGCAGCGAGCTGCGAG 25173
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RESULT 6
US-09-927-091-4
; Sequence 4, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILMAY, ANN
; APPLICANT: LLOYD, STEVE
; APPLICANT: CHANDLER, DAMN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 49744
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-4

Query Match 21.9%; Score 838.6; DB 10; Length 49744;
Best Local Similarity 93.5%; Pred. No. 7e-220;
Matches 951; Conservative 0; Mismatches 59; Indels 7;

QY 1 AGGCTGCGCTGAGACCGAAGCGGTGCTTAAAGTCCGCGGGTTAAGGGTCCGCGTGG 60
| | | | |
Db 34306 AGGCTGCGCTGAGACCGAAGCGGTGCTTAAAGTCCGCGGGTTAAGGGTCCGCGTGG 34365
| | | | |
QY 61 CCAAGGTTTGGGCGCGGATTCGGGACAGTCAAGGCGGCGGACCCCTCTCTCTGCTGCG 120
| | | | |
Db 34366 CCA-GGTTTGGGCGCGGATTCGGGACAGTCAAGGCGGCGGACCCCTCTCTCTGCTGCG 34424
| | | | |
QY 121 GGTACAGCAATGTAGGGTCCGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 180
| | | | |
Db 34425 GGTACAGCAATGTAGGGTCCGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 34484
| | | | |
QY 181 GCTTCTGCGCTCCCGCCACCGCGCCCGCCCGCGGATTTGAGACCCCTTAAAGGCTCCAC 240
| | | | |
Db 34485 GCTTCTGCGCTCCCGCCACCGCGCCCGCCCGCGGATTTGAGACCCCTTAAAGGCTCCAC 34544
| | | | |
QY 241 CCGGCTCGGGGATCCCTTCTCCAGCTCTTATCCCTTAAAGACTGCGCGCGCTGAGAA 300
| | | | |
Db 34545 CCGGCTCGGGGATCCCTTCTCCAGCTCTTATCCCTTAAAGACTGCGCGCGCTGAGAA 34604
| | | | |
QY 301 CTTCCCG-CTACAGGATCTCGGTC-CTTACAGCGCTGACA-GCTTCTCCAGCGCGCCATC 357
| | | | |
Db 34605 CTTCCCGAGTTAGGATCTCGGTCCTTACAGCGCGCTGACA-GCTTCTCCAGCGCGCCATC 34664
| | | | |
QY 358 GCC-TTGAGCTGCGCACTACC-TCTAAGCTGCGCTCCCGGCTGCGGCTCCACGAGTCT 415
| | | | |
Db 34665 GCC-TTGAGCTGCGCACTACC-TCTAAGCTGCGCTCCCGGCTGCGGCTCCACGAGTCT 34724
| | | | |
QY 416 CAGCGCGGACCCCTTCTGCGGTTACCTTCTTCCGAGACAGACCCCTTCTGCGG 475
| | | | |
Db 34725 CAGCGCGGACCCCTTCTGCGGTTACCTTCTTCCGAGACAGACCCCTTCTGCGG 34784
| | | | |
QY 476 GTAGCTCTTACCCCTGCTGAGGCGGCTGTCGCCGCGGCGAGCCCTGCTGCTGCTG 535
| | | | |
Db 34785 GTAGCTCTTACCCCTGCTGAGGCGGCTGTCGCCGCGGCGAGCCCTGCTGCTGCTG 34844
| | | | |
QY 536 CGACAGCGGCGG-CCCTCTACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 594
| | | | |
Db 34845 CGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 34904
| | | | |
QY 595 CTTGCGGCGGCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 654
| | | | |
Db 34905 CTTGCGGCGGCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 34964
| | | | |
QY 655 TACAGGAGCCGCGGAGCTGAGGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 714
| | | | |
Db 34965 TACAGGAGCCGCGGAGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 35024
| | | | |
QY 715 CACTGGGTGCGGAGAGGCGGAGGCGGCGGCGGAGCTGCCGAGAGTCCGCGGAGGTTG 774
| | | | |
Db 35025 CACTGGGTGCGGAGAGGCGGAGGCGGCGGCGGAGCTGCCGAGAGTCCGCGGAGGTTG 35084
| | | | |
QY 775 GCGGAGCGGCGGCTGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834
| | | | |
Db 35085 GCGGAGCGGCGGCTGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 35144
| | | | |
QY 835 TTCGCGGTGAGAGCACTCTCAAGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 894
| | | | |
Db 35145 TTCGCGGTGAGAGCACTCTCAAGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 35204
| | | | |
QY 895 AAGTCAAGCTCTTCTGCTACAGGAGCGGCGGCTTCTGCTTCTTCTGCGAGAGGCT 954
| | | | |
Db 35205 AAGTCAAGCTCTTCTGCTACAGGAGCGGCGGCTTCTGCTTCTTCTGCGAGAGGCT 35264
| | | | |
QY 955 GCACTGACAGAGAGAGATCAGGCTCAGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1011
| | | | |
Db 35265 GCACTGACAGAGAGAGATCAGGCTCAGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 35321
| | | | |
RESULT 7
US-10-027-632-100265/c
; Sequence 100265, Application US/10027632

Query Match 14.7%; Score 562; DB 9; Length 573;
Best Local Similarity 99.8%; Pred. No. 1.4e-144;
Matches 573; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1602 CTTGATGTGAGGTGTCGTGGTGTCTGAAGCCTTCAATGATGTCGCTCACTATG 1661
DB 573 CTTGATGTGAGGTGTCGTGGTGTCTGAAGCCTTCAATGATGTCGCTCACTATG 514
QY 1662 GGAAGTGTGTGTCGCGAGAAAGACCAAGTGGGTATCGGGCTGCACAGAGCGCAG 1721
DB 513 GGAAGTGTGTGTCGCGAGAAAGACCAAGTGGGTATCGGGCTGCACAGAGCGCAG 454
QY 1722 CCGCAAGGCGCAGATCCAGATCCAGCCCGCGGCTTCTACATGATCGTGAAGCAGA 1781
DB 453 CCGCAAGGCGCAGATCCAGATCCAGCCCGCGGCTTCTACATGATCGTGAAGCAGA 394
QY 1782 TGACACAGTACAGCGCTCTGACAGAGCCCTGAGAGCGGCTTAAAGTCGCGGACAACT 1841
DB 393 TGACACAGTACAGCGCTCTGACAGAGCCCTGAGAGCGGCTTAAAGTCGCGGACAACT 334
QY 1842 TGACAGGTGGTGTCTTCTGACTATGACCAAGGCTTGTCTCATCTTCAATGTCTGA 1901
DB 333 TGACAGGTGGTGTCTTCTGACTATGACCAAGGCTTGTCTCATCTTCAATGTCTGA 274
QY 1902 TGACATGCTGCTGCTACACCTTCCGCGAAGATTCCTGCGCAAGCTCTCTTACTT 1961
DB 273 TGACATGCTGCTGCTACACCTTCCGCGAAGATTCCTGCGCAAGCTCTCTTACTT 214
QY 1962 CAGCCCTGCGCAGAGCCAGCCCAATGCGAAGAGTTCAGCGCTGCGGATCAACACCGT 2021
DB 213 CAGCCCTGCGCAGAGCCAGCCCAATGCGAAGAGTTCAGCGCTGCGGATCAACACCGT 154
QY 2022 CCGCATCTAGTCCAGGAGAAAGAGACCAACCTCCTGGAGCACTGCGACCTGCAAGA 2081
DB 153 CCGCATCTAGTCCAGGAGAAAGAGACCAACCTCCTGGAGCACTGCGACCTGCAAGA 94
QY 2082 GCCCTGCCAGGAAGATAGAAAGACCTGACTCCAGCCCAAGCTGGCCACTGGAAGCTCA 2141
DB 93 GCCCTGCCAGG -AGATAGAAAGACCTGACTCCAGCCCAAGCTGGCCACTGGAAGCTCA 35
QY 2142 GGCAGTGTGTATCCCTCCAGCTCCAGTCTGA 2175
DB 34 GGCAGTGTGTATCCCTCCAGCTCCAGTCTGA 1

RESULT 9
US-09-864-761-23962/c
; Sequence 23962, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemolca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23962
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC02262.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EST_HUMAN HIT: BE315402.1, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q02084, EVALUATE 5.00e-28
; OTHER INFORMATION: NT HIT: g11423970, EVALUATE 0.00e+00
US-09-864-761-23962

Query Match 11.3%; Score 431; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GTAGTGGCTCCACTACTGAGAGGTGTGGTGGGGAAGAACCCAGTGGTATCGGGC 1702
DB 431 GTAGTGGCTCCACTACTGAGAGGTGTGGTGGGGAAGAACCCAGTGGTATCGGGC 372
QY 1703 TGGCACAGAAAGCCGCAAGGCGCAAGGAGCATCCAGATCCAGCCAGCGGCTTCT 1762
DB 371 TGGCACAGAAAGCCGCAAGGCGCAAGGAGCATCCAGATCCAGCCAGCGGCTTCT 312
QY 1763 ACTGCATGTGATGACAGATGAGCAACGATACAGCCCTGCGAGAGCCCTGAGCGGGC 1822
DB 311 ACTGCATGTGATGACAGATGAGCAACGATACAGCCCTGCGAGAGCCCTGAGCGGGC 252
QY 1823 TTACGTCGCGGAGAAAGCTTGACAAAGTGGGTGTCTTCTCGACTATGACCAAGCTTGC 1882
DB 251 TTACGTCGCGGAGAAAGCTTGACAAAGTGGGTGTCTTCTCGACTATGACCAAGCTTGC 192
QY 1883 TCATCTTCAATAGTATGATGATGTCGTGCTCTACACCTTCCGAGAGTTCCTG 1942
DB 191 TCATCTTCAATAGTATGATGATGTCGTGCTCTACACCTTCCGAGAGTTCCTG 132
QY 1943 GCAAGCTGTGCTTACTTACAGCCCTGCGCAGAGCCAGCCCAATGGAAGAAGCTTACG 2002
DB 131 GCAAGCTGTGCTTACTTACAGCCCTGCGCAGAGCCAGCCCAATGGAAGAAGCTTACG 72
QY 2003 CGCTGCGGATCAACCGCTCGCATCTAGTCAAGGAGAAAGAGACCAACCACTCTGGG 2062

QY 817 GTGGAGCGCTACAGCTCTCCCGCTGGAGCCCATCTCAAGCGCGCGCGCGCA 876
DB 4569 CC 4510
QY 877 CCCTGCCAGGCGGACGACAAG 898
DB 4509 CCCCCCCCCCCCCCACTTCAAG 4488

RESULT 14

US-10-032-393-8/c
Sequence 8, Application US/10032393
Publication No. US20030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12739
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Vector pPEPFI
US-10-032-393-8

Query Match 3.2%; Score 122; DB 14; Length 12739;
Best Local Similarity 47.0%; Pred. No. 2.7e-22;
Matches 377; Conservative 0; Mismatches 425; Indels 0; Gaps 0;

QY 97 CCGGACCCCTCTCTCTCTGCGGCTGACAGCAATGTAAGCGCTGGCTGGCTGCC 156
DB 5295 CC 5236
QY 157 CTCGCCAGAGTAATCCCATCCCGAGCTTCGCGCTCCCGGACCGCGCGGGA 216
DB 5235 CC 5176
QY 217 TTTCGACCCCTTAAGAGGCTCAACCCGCTCCGGATCCCTTCTCCAGCTCTATCC 276
DB 5175 CC 5116
QY 277 TTAGAGCTGCGCGCGCGCTAGAGCTCCCGTAGAGATCTCGCTCCCTAGCGCTAC 336
DB 5115 CC 5056
QY 337 AGCTCTCCGACGCGCAATCGCTTGAAGTCCCACTATCTTGAAGTGGCGCGG 396
DB 5055 CC 4996
QY 397 CTGGGCTCCAGAGCTTCAGCGGCAACCCCTTCCGCTGATACCTCTTCGAGCA 456
DB 4995 CC 4936
QY 457 GCAACCCCTCTCTCTCCGTAAGCTTCAACCTGCTGCGGCTGCTCCCGGCGC 516
DB 4935 CC 4876
QY 517 CAGCGCTGGTGTGCTCCGACAGGCGCGGCTCTCTAGCGCGCGCGCGCTGCGG 576
DB 4875 CC 4816

QY 577 GCCCCCTCTCTGCTGCCCTTGCGCCATGAGCGGTGCAAGCTCAAGAGAGCTGTGC 636
DB 4815 CC 4756
QY 637 TCCATGTGCTTGAAGCATCTACAGAGACCGGATAGCTGGGCTGCGAGCACTTCTGC 656
DB 4755 CC 4696
QY 697 CGCGGCTGATCAAGGAGCATGTGGGTCGCGAGAGGCGGAGGCGCGCGAGCTGCCC 756
DB 4695 CC 4636
QY 757 GAGTCCGCGGCAAGTTCGCGGAGCCCGGCTGAGCGCCAGCTCAAGTGGCCAAATC 816
DB 4635 CC 4576
QY 817 GTGGAGCGCTACAGCTCTTCCGCTGGAGCGCATCTCAAGCGCGCGCGCGCGGA 876
DB 4575 CC 4516
QY 877 CCCTGCCAGGCGGACGACAAG 898
DB 4515 CCCCCCCCCCCCCCACTTCAAG 4494

RESULT 15

US-10-137-870-123
Sequence 123, Application US/10137870
Publication No. US20030138883A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C155
CURRENT APPLICATION NUMBER: US/10/137,870
PRIOR FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 123
LENGTH: 3479
TYPE: DNA
ORGANISM: Homo Sapien
US-10-137-870-123

Query Match 3.1%; Score 119.2; DB 12; Length 3479;
Best Local Similarity 52.4%; Pred. No. 7.8e-22;
Matches 262; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 1484 CAGCCGCTTAACCTTGACCCGCGGACAGCCACAGCGCTGATCTGTGAGACT 1543
DB 1197 CAGTGATGTGAGAGCTGACCGGCTCGGCGAGACCCAGACTGAGAGTCCGAGATG 1256
QY 1544 GCAACATTTGGCTTACGCACTTGACCCAGACGACGACGAGAGTCCCAAGGCT 1603
DB 1257 GCAAGAGCTGTCTTCCCGGCGGCGCGGAGCGCGGCGGCTGAGCAACCGAGCGGT 1316

QY	1604	TCGATGTGGAGAGTGTCCGGTGGCTGGGTTTCTGAAGCTTCAGTATGAGGGTCCACATACATAGG	1653
Db	1317	TCCTGGAGACAGACATGCGCGCTGAGCCTGGAGCGGATTCCTCCGCGGCGCCGACCTACTAGGG	1376
QY	1664	AGGTGTGGTGGCGGAGNAGNACCCAGTGGGATCGGGCTGGCACAGNAGCCGCAAGCC	1723
Db	1377	AGGTGACAGTGGGCGCGCCGACAGCCGCTGTGGTTCCTGTGGGCGCCTGGCTGGCGCGGGTGGCCG	1436
QY	1724	GCAAGGCGAGCATCCAGATCCAGAGCCGACCGCGGCTTCTACTGCATGCTATGACAGATG	1783
Db	1437	GCGCGGGGCGCTGCGCGGCTGAGCCCTGGCGCGGCTACTTGGGTTCTGGGGCTGTGGNAGC	1496
QY	1784	GCAACACAGTACAGCGGCTGCACAGGAGCCCTGGAGCGGCTTAAAGCTCCGGGACCAAGCTTG	1843
Db	1497	GCTCGAGATACTTGTGCTCTGGCCCCCGCACCGCGCTGCGGCTACCTTGCGGCTGCCCGCC	1556
QY	1844	ACAAGTGGGATGTCTCTCTGGACATATGACCAAGGCTTGCTATCTTCTACATAGCTGATG	1903
Db	1557	GCGCGCTGGGCGGTCTTCCTGTGACATACAGAGCGCGGAGAGCTGTCTTCTTCAAGCTGTCCG	1616
QY	1904	ACATGTCTTGCTCTACACCTTCGCGGAGAAATTCCCTGGGACGCTGCTCTTACTTCA	1963
Db	1617	ACGGCTCCCACTTTCACCTTCCACGACACCTTCTGGGGCGGCTGTGTGCTACTTCA	1676
QY	1964	GCCTGGGCGACAGGCAGGCC	1983
Db	1677	GGCCCAAGGCGCCACGACGCG	1686

Search completed: October 9, 2003, 00:43:42
Job time : 955 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 15:01:47 ; Search time 13564 Seconds

(without alignments)
11539.386 Million cell updates/sec

Title: US-09-927-091-3

Perfect score: 3826
Sequence: 1 aggcgcgcctgcgcgaagc.....aaaaaaaaaaaaaaaaaaaaa 3826

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 segs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenEmbl:*
2: gb_da:*
3: gb_htg:*
4: gb_in:*
5: gb_om:*
6: gb_ov:*
7: gb_ph:*
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13: gb_un:*
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30: em_htg_hum:*
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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3826	100.0	3826	6	AX491279
2	3420.2	89.4	3436	6	BD156501
3	3420.2	89.4	3436	9	AK001621
4	3232	84.5	3259	9	BC001222
5	3232	84.5	3259	9	BC007999
6	3232	84.5	3259	9	BC012152
7	3232	84.5	3259	9	BC011689
8	2322.2	60.7	23433	6	AX491283
9	2322.2	60.7	164950	2	AC022262
10	2320.6	60.7	64693	2	AL662907
11	2308.6	60.3	30676	6	AX491284
12	2295.8	58.9	136095	2	AF161326
13	2252.8	58.9	30625	6	AX491281
14	1394.2	36.4	3216	10	BC049095
15	995.8	26.0	45845	6	AX491282
16	917.2	24.0	136095	2	AF161326
17	838.6	21.9	49744	6	AX491280
18	642	16.8	264606	2	AC137264
19	612.8	16.0	193830	10	AL607086
20	592.2	15.5	628	6	BD148776
21	520.4	13.6	557	6	BD153810
22	230	6.0	250	11	G15084
23	179.4	4.7	1461	4	AY081951
24	170.8	4.5	2044	9	AY081949
25	166.4	4.3	2047	9	AY081948
26	161.2	4.2	3102	10	AB046382
27	160.6	4.2	2948	10	BC031540
28	160.4	4.2	2343	5	S80988
29	160.2	4.2	2045	6	AX714775
30	160.2	4.2	2045	9	AK057366
31	155.6	4.1	2115	5	BC047956
32	155.4	4.1	1467	9	BT007370
33	155.4	4.1	1467	12	BT007627
34	155.4	4.1	3128	9	BC007661
35	153.8	4.0	3551	9	BC034985
36	152.4	4.0	2253	5	XELXNF7A
37	152.4	4.0	2253	5	S64515
38	146.2	3.8	2526	5	SMRPWA33A
39	139.2	3.6	2597	6	AX600203
40	138.8	3.6	2714	9	AF327056
41	136.4	3.6	38093	9	AB014085
42	136.4	3.6	46692	9	AC004187
43	136.4	3.6	88074	9	AL773535
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ALIGNMENTS

RESULT 1
AX491279
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX491279 3826 bp DNA linear PAT 16-AUG-2002
Sequence 3 from Patent WO0212285.
AX491279
AX491279.1 GI:223233980
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Killary,A., Chandler,D. and Lott,S.
The tumor suppressor car-1
Patent: WO 0212285-A 3 14-FEB-2002;

Pred. No. is the number of results predicted by chance to have a

BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)

FEATURES	Location/Qualifiers
source	1. . 3826

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/organism="Homo sapiens"  
/mol_type="genomic DNA"  
/db_xref="taxon:9606"
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ORIGIN				

Query Match	100.0%	Score 3826;	DB 6;	Length 3826;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3826; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

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Db	1	AGGCTGGGCTGGAGCGAAGCGGTGGCTCTAAAGCTGGGGGGGTTAAGGGGTTCGGCTGGG	60
OY	61	CCAGGGTTTGGGGCCGGGATCCGGAGCTGAGCGGGCCGGACCCCTCTCTTCTCTGCC	120
Db	61	CCAGGGTTTGGGGCCGGGATCCGGAGCTGAGCGGGCCGGACCCCTCTCTTCTCTGCC	120
OY	121	GGTCACAGCCAAATTAGGGCTCGGGCTTGCGTGGCCCCCTCCCCAAGATTCCCATCCCCA	180
Db	121	GGTCACAGCCAAATTAGGGCTCGGGCTTGCGTGGCCCCCTCCCCAAGATTCCCATCCCCA	180
OY	181	GCTTCTGGCCCTCCCGCAGCCGGCCCAACCCCGGGATTTCAGACCCCTCTTAAGGGCTCCAC	240
Db	181	GCTTCTGGCCCTCCCGCAGCCGGCCCAACCCCGGGATTTCAGACCCCTCTTAAGGGCTCCAC	240
OY	241	CCGCGCTCCGGGATCCCTTCTCCAGAGCTCTATCCCTTAAGAGCTGCCCGGCCCTTAGAA	300
Db	241	CCGCGCTCCGGGATCCCTTCTCCAGAGCTCTATCCCTTAAGAGCTGCCCGGCCCTTAGAA	300
OY	301	CTCTCCCGGTAGAGATTCGCTCCCTCAAGCGGCTCAAGCCCTCTCCAGCGGCCCATGGCC	360
Db	301	CTCTCCCGGTAGAGATTCGCTCCCTCAAGCGGCTCAAGCCCTCTCCAGCGGCCCATGGCC	360
OY	361	TTAGAGCTGCCACTACCTCTAGACTGCGCCTCCGGGGCTGGCGTCCCAAGAGTCTCAACC	420
Db	361	TTAGAGCTGCCACTACCTCTAGACTGCGCCTCCGGGGCTGGCGTCCCAAGAGTCTCAACC	420
OY	421	GGGACCCCTTCCTCGGGTTACCTCTCTCCGGAGACAGACCCCTCCCTTTCGGGTAGC	480
Db	421	GGGACCCCTTCCTCGGGTTACCTCTCTCCGGAGACAGACCCCTCCCTTTCGGGTAGC	480
OY	481	TCTACACCCCTGCTGTCGGGGCTCTGTCGCCGCGCCAGACCCCTCGGTCTGCTCCGACA	540
Db	481	TCTACACCCCTGCTGTCGGGGCTCTGTCGCCGCGCCAGACCCCTCGGTCTGCTCCGACA	540
OY	541	GGGCGGGCTCTCAAGCCGGCCCCCTTGGGGCCCTCGCTGCTGCTGGCCCTGGC	600
Db	541	GGGCGGGCTCTCAAGCCGGCCCCCTTGGGGGCCCTCTGCTGCTGGCCCTGGC	600
OY	601	GCCATGGCGTGAACCTCAAGAGAGAGTGTGTGTCATCTGACCTGAGATCTACACG	660
Db	601	GCCATGGCGTGAACCTCAAGAGAGAGTGTGTGTCATCTGACCTGAGATCTACACG	660
OY	661	GACCGGGTGAAGCTGGGCTCGAGACACTTCTGCGCGGCTGCATCACGGACACTGG	720
Db	661	GACCGGGTGAAGCTGGGCTCGAGACACTTCTGCGCGGCTGCATCACGGACACTGG	720
OY	721	GTCGGGAGAGAGGGGCGAGGGGGCCCGGACTGCCCCGAGTGCGGGCGACGTTGGCGAG	780
Db	721	GTCGGGAGAGAGGGGCGAGGGGGCCCGGAGCTGCCCCAGTGCGGGCGACGTTGGCGAG	780
OY	781	CCGCGGCTGGAGCGCCACTCAAGCTGAGCAACATCTGGAGCGCTAGCTTCCTTCCG	840
Db	781	CCGCGGCTGGAGCGCCACTCAAGCTGAGCAACATCTGGAGCGCTAGCTTCCTTCCG	840
OY	841	CTGAGAGCAATCTCTCAACGCGCGCGCGCGCGGACCTTCCACAGGCGCAAGACAAGTTC	900
Db	841	CTGAGAGCAATCTCTCAACGCGCGCGCGCGCGGACCTTCCACAGGCGCAAGACAAGTTC	900

QY	901	AAGCTCTTCTGCTACAGGACCGGGCGCTTCTCTGCTTCTTCTGCGAGAGACTGCAC	CTG	960
Db	901	AAGCTCTTCTGCTCTACGAGACCGGGCGCTTCTCTGCTTCTTCTGCGAGAGACTGCAC	CTG	960
QY	961	CAGGACGACATCAGTCAACCGGATCAGCAACGCTTGCAGAGCTGACAGAGGACTG	1020	
Db	961	CAGGACGACATCAGTCAACCGGATCAGCAACGCTTGCAGAGCTGACAGAGGACTG	1020	
QY	1021	AAGGACCAACTTCAGGCGCTTCCAGACAGCGAGGGGAAACACCCGAAGCGCTGCAC	CTG	1080
Db	1021	AAGGACCAACTTCAGGCGCTTCCAGACAGCGAGGGGAAACACCCGAAGCGCTGCAC	CTG	1080
QY	1081	CTCAAGCAACAATGGCGGAGACCAAGCTTCCACCAAGAGCTGCGGACACTATGAGG	1140	
Db	1081	CTCAAGCAACAATGGCGGAGACCAAGCTTCCACCAAGAGCTGCGGACACTATGAGG	1140	
QY	1141	GAGGCGTTGAGAGCGGCTGCACCGCTGCTGCTGAGAGCGCCGAAAGGCCATGCTAGAG	AG	1200
Db	1141	GAGGCGTTGAGAGCGGCTGCACCGCTGCTGCTGAGAGCGCCGAAAGGCCATGCTAGAG	AG	1200
QY	1201	CTGGAGGGGGAGACGGCGCCGACGCTGACGCAATCCAGACGAAGAAAGTCCAGCGCTAC	AGC	1260
Db	1201	CTGGAGGGGGAGACGGCGCCGACGCTGACGCAATCCAGACGAAGAAAGTCCAGCGCTAC	AGC	1260
QY	1261	CAGCAGCTGCGCAAGGTCCAGAGAGGAGACCAGATCCTGCGAGAGCGGCTGCGTGA	AAC	1320
Db	1261	CAGCAGCTGCGCAAGGTCCAGAGAGGAGACCAGATCCTGCGAGAGCGGCTGCGTGA	AAC	1320
QY	1321	GACCGGGCAACCTTCTTGCTGGGCTGGGCTCTCATCTGTCGAGCGGCTCCAGGGAA	AATC	1380
Db	1321	GACCGGGCAACCTTCTTGCTGGGCTGGGCTCTCATCTGTCGAGCGGCTCCAGGGAA	AATC	1380
QY	1381	CATGAGACCAACTCATATGAAAGACTCCCGACCTCCAAATGACAGAGCGCCCTG	CAG	1440
Db	1381	CATGAGACCAACTCATATGAAAGACTCCCGACCTCCAAATGACAGAGCGCCCTG	CAG	1440
QY	1441	TACACATCTGGAAGTCCCTGTCCAGAGACATCCACCAGTCCAGCGCCCTTAACCTG	1500	
Db	1441	TACACATCTGGAAGTCCCTGTCCAGAGACATCCACCAGTCCAGCGCCCTTAACCTG	1500	
QY	1501	GACCGGGCAAGGCCCAACAGCGGCTGATCCTGCGAGACGACTGCACATTTGGCGCTTAC	1560	
Db	1501	GACCGGGCAAGGCCCAACAGCGGCTGATCCTGCGAGACGACTGCACATTTGGCGCTTAC	1560	
QY	1561	GGCACCTTGCACCCACAGCACTCAGAGACTCGCCAAAGCGCTTCGATGTGAGAGTGC	1620	
Db	1561	GGCACCTTGCACCCACAGCACTCAGAGACTCGCCAAAGCGCTTCGATGTGAGAGTGC	1620	
QY	1621	GTCGCGGTTCTGAAAGCCTTCAGTAAAGTGGGCTCCACTACGTGGAGAGTGGTGGCGGAG	1680	
Db	1621	GTCGCGGTTCTGAAAGCCTTCAGTAAAGTGGGCTCCACTACGTGGAGAGTGGTGGCGGAG	1680	
QY	1681	AAGACCCAGTGGTATCGGGCTGGCAACAGAACCCGCAAGCGCAAGGGCAGACTACAG	1740	
Db	1681	AAGACCCAGTGGTATCGGGCTGGCAACAGAACCCGCAAGCGGACAGATCCAG	1740	
QY	1741	ATCCAGCCCAACCGCGGCTTACTGATGATGTATGACATGGCAACAGTACAGCGCC	1800	
Db	1741	ATCCAGCCCAACCGCGGCTTACTGATGATGTATGACATGGCAACAGTACAGCGCC	1800	
QY	1801	TGCAGAGAGCCTTGAGAGCGGCTTAAGTCCGGAGACAAGCTTGACAAAGTGGGTGTC	1860	
Db	1801	TGCAGAGAGCCTTGAGAGCGGCTTAAGTCCGGAGACAAGCTTGACAAAGTGGGTGTC	1860	
QY	1861	CTGGACTATGACCAAGGCTGCTCATCTTCTACAAATGCTGATGACATGCTGCTGC	CTAC	1920
Db	1861	CTGGACTATGACCAAGGCTGCTCATCTTCTACAAATGCTGATGACATGCTGCTGC	CTAC	1920
QY	1921	ACCTTCCGGGAGAGTTCCTTGGCAACCTGCTCTTACTTACAGCCTTGCCAGAGAC	CAC	1980
Db	1921	ACCTTCCGGGAGAGTTCCTTGGCAACCTGCTCTTACTTACAGCCTTGCCAGAGAC	CAC	1980
QY	1981	GCCAAATGGCAAGACGTTACAGCGCTCGGATCAACACGCTCCGCACTCTAGTCCAGGAG	2040	

Db 1981 GCGAATGGCAAGACGTTAGCCGCTGGGATACACCGCTCCGCACTGATGTCAGAGCA 2040
 Oy 2041 AAGGAGACCACAACCTCTCTGGGACCACTGCCACTTCAGAGAGCCCTGCCAGAAATAT 2100
 Db 2041 AAGGAGACCACAACCTCTCTGGGACCACTGCCACTTCAGAGAGCCCTGCCAGAAATAT 2100
 Oy 2101 AAGACCTGGACTCCAGCCACCGTGGCCACTGGAGACTCCAGGCACTGTTTACCCTCC 2160
 Db 2101 AAGACCTGGACTCCAGCCACCGTGGCCACTGGAGACTCCAGGCACTGTTTACCCTCC 2160
 Oy 2161 AAGCTCCAGTCTGTAAATGAGAGGTGATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220
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 Oy 2221 GATGTTCTGTAGCTCTGACCTTGATAGGATACAGTTTATGATCCAGAGATGATGATG 2280
 Db 2221 GATGTTCTGTAGCTCTGACCTTGATAGGATACAGTTTATGATCCAGAGATGATGATG 2280
 Oy 2281 TTCTCTCAGGCAACCCCTGCCCAACCTCATCCCATCTCTCTCTCTCTCTCTCTCTCTCT 2340
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 Oy 2341 CCTTCAGTCT 2400
 Db 2341 CCTTCAGTCT 2400
 Oy 2401 AGTTGGCAGCCCGAAAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2460
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 Oy 2461 TGAACCAAGTATGATGGCCATTACCTTGACCCAGTCCAGTGGTCTACAGGTAGT 2520
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 Oy 2521 AACTGGTCTAGGAGTGGCTGAGAGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
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 Oy 2581 ATGTTCT 2640
 Db 2581 ATGTTCT 2640
 Oy 2641 CACCTGGTATGTTGATGTCACACATTATAGTATGTCACACACCTCTCTCTCTCTCTCTCT 2700
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 Oy 2701 GAGGAGACGGGTGAGGATATCCCAAGCTGATGACAGAGCCATTAGCTTAAAGCAACT 2760
 Db 2701 GAGGAGACGGGTGAGGATATCCCAAGCTGATGACAGAGCCATTAGCTTAAAGCAACT 2760
 Oy 2761 GCAGAGCAAGCCTCCCTGATGATCGAGGTCCCACTAGCTCTGAAACAAGATCCAGCA 2820
 Db 2761 GCAGAGCAAGCCTCCCTGATGATCGAGGTCCCACTAGCTCTGAAACAAGATCCAGCA 2820
 Oy 2821 ACCCTCTTACAGCAGGCTCTGTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
 Db 2821 ACCCTCTTACAGCAGGCTCTGTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
 Oy 2881 TTGTATTTAGGACCAAGCACTGGGAGGGGCTGTTGGCTAGAGCCCTTCTGACACTGGC 2940
 Db 2881 TTGTATTTAGGACCAAGCACTGGGAGGGGCTGTTGGCTAGAGCCCTTCTGACACTGGC 2940
 Oy 2941 ATCTATCTCAGTTAGATCTCTCTGAGAAACAAGAGCAGCTTGTAGCTGTTTAAATTA 3000
 Db 2941 ATCTATCTCAGTTAGATCTCTCTGAGAAACAAGAGCAGCTTGTAGCTGTTTAAATTA 3000
 Oy 3001 GACAAAGATTTACTACTCTGCCCCCTGTGGCTTGAACAAATTTGTTGGAAGAGCTGGAAG 3060
 Db 3001 GACAAAGATTTACTACTCTGCCCCCTGTGGCTTGAACAAATTTGTTGGAAGAGCTGGAAG 3060
 Oy 3061 GAGACTCTGCTGAATTTCCAGGAACCTCCAGGCCAGATTCAATCATGTCTGTTGTACCA 3120
 Db 3061 GAGACTCTGCTGAATTTCCAGGAACCTCCAGGCCAGATTCAATCATGTCTGTTGTACCA 3120

Db 3061 CAGACTCTGCTGAATTTCCAGGACTCCAGGCCCAAGATTCATGATGCTGTTGTACCA 3120
 Oy 3121 GGAAGCTGCCCCCATCTGAGAGAGCCATATGACAGAAAGCTGCTGATGAGACTA 3180
 Db 3121 GGAAGCTGCCCCCATCTGAGAGAGCCATATGACAGAAAGCTGCTGATGAGACTA 3180
 Oy 3181 GGTCTCTCTGCCAGGCTCCGTGACAGCCAAATGATGCTGAGGCTGCCCCCTGCCA 3240
 Db 3181 GGTCTCTCTGCCAGGCTCCGTGACAGCCAAATGATGCTGAGGCTGCCCCCTGCCA 3240
 Oy 3241 CTTCACCTGATCCCAATCTAAATTTTACAAAGATTCCTGTTGGGGAACTTAAATG 3300
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 Oy 3361 GGTGGGTGGAGCAAGCCCACTGCTGTTTCTGACAGATCCAAATCTGMAAGACT 3420
 Db 3361 GGTGGGTGGAGCAAGCCCACTGCTGTTTCTGACAGATCCAAATCTGMAAGACT 3420
 Oy 3421 CGGAGAGGGTGGAGTCCACATCTAGGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3480
 Db 3421 CGGAGAGGGTGGAGTCCACATCTAGGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3480
 Oy 3481 AGTGGGAATCTGAGAGAGTGGGCTGCAAGACTAGCCTTAAATGCTCTCTCTCTCTCTCT 3540
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 Db 3661 GGCCTCTCTTGGGCAAAAGAAATTTGACAGCCCTTAAACCTTCAACTACAGAAATCT 3720
 Oy 3721 GGGCAACCCAGCAGATTTTAAATGTTGAGGCTTAAATGATGATGATCAAT 3780
 Db 3721 GGGCAACCCAGCAGATTTTAAATGTTGAGGCTTAAATGATGATGATCAAT 3780
 Oy 3781 TGTATTAATTAATTAAGTTACAGATGTCATCAATCAATCAATCAATCAATCAATCAAT 3840
 Db 3781 TGTATTAATTAATTAAGTTACAGATGTCATCAATCAATCAATCAATCAATCAATCAAT 3840

RESULT 2
 BD156501 3436 bp DNA linear PAT 17-JAN-2003
 LOCUS DEFINITION
 BD156501 Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION
 BD156501.1 GI:27862259
 VERSION JP 2002191363-A/11344.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3436)
 Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.,
 Primer for synthesizing full-length cDNA and use thereof
 JOURNAL
 TITLE
 JOURNAL
 COMMENT
 OS Homo sapiens (human)
 PN JP 2002191363-A/11344
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU

	PI	SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ 10, PC C12P1/02, C12Q1/68//C12P1/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key	
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SOURCE			1..3436 "/organism='Homo sapiens' /'mol_type='genomic DNA' '/db_xref='taxon:9606'
BASE COUNT			731 a 1126 c 901 g 678 t
ORIGIN			
Query Match			89.4% Score 3420.2; DB 6; Length 3436;
Best Local Similarity			99.9%; Pred. No. 0;
Matches 3433:			Conservative 0; Mismatches 3; Indels 1; Gaps 1.
Oy	370	CCACACTCTAGAATGCGCTTCGCCGGGTGGGGTGCACAGAGATCTACGCCGGCACCCC	429
Dd	1	CCACACTCTAGAATGCGCTTCGCCGGGTGGGGTGCACAGAGATCTACGCCGGCACCCC	60
Oy	430	TTCCTGCGATTACCCTCCCTCCGGACAGACACCCCCCTCCCTTCCTCCGTAAGTCTCAACC	489
Dd	61	TWCCTCGGGTTAACCTCTCCCGGACACACCCCTCCCTTCCTCCGTAAGTCTCAACC	120
Oy	490	TGCCGTGTCGGGGCCGTCCCGGSCCAAGCCCTTGGTGTCTCTCCGACAGCGCGCGC	549
Dd	121	TGCCGTGTCGGGGCCGTCCCGGSCCAAGCCCTTGGTGTCTCTCCGACAGCGCGCGC	180
Oy	550	TCTCTCAGACCCGCCCTGCCCCGTGGGGCCCCCTCTGCTGGTGCCCCGCGCATATGCG	609
Dd	181	TCTCTCAGACCCGCCCTGCCCCGTGGGGCCCCCTCTGCTGGTGCCCCGCGCATATGCG	240
Oy	610	TGCAGCTCAAGAGACGAAGCTGCTGTGTCTCATTCTGCTAGCATCTACAGAGACCGGTG	669
Dd	241	TGCAGCTCAAGAGAGACGAAGCTGCTGTGTCTCATTCTGCTAGCATCTACAGAGACCGGTG	300
Oy	670	AGCGGGGGCTGGAGACAATACTTCGCGCGCGGCTGATCAGAGAACTGGGTGGGGAG	729
Dd	301	AGCGGGGGCTGGAGACAATACTTCGCGCGCGGCTGATCAGAGAACTGGGTGGGGAG	360
Oy	730	GAGGGGAGGGGCGCGGAGCTGCCCCAGTAGTGCGGCGCACGTTTGCGGACCGCGCTG	789
Dd	361	GAGGGGAGGGGCGCGGAGCTGCCCCAGTAGTGCGGCGCACGTTTGCGGACCGCGCTG	420
Oy	790	GCGGCCAAGCTCAAGCTGGCCAATGCTGGAGCGCTACAGCTCTCCCTGTGAGCGCC	849
Dd	421	GCGGCCAAGCTCAAGCTGGCCAATGCTGGAGCGCTACAGCTCTCCCTGTGAGCGCC	480
Oy	850	ATCCCAAGCGGGCGCGGCGGAGACCCGTGCAAGGGGACAGCAAGGTCAAAGTCTTC	909
Dd	481	ATCCCAAGCGGGCGCGGCGGAGACCCGTGCAAGGGGACAGCAAGGTCAAAGTCTTC	540
Oy	910	TGCCCTCAGGAGCGGCGCTCTCGCTGCTTCCTTGCGAGAGCGCTGCACTGACAGAG	969
Dd	541	TGCCCTCAGGAGCGGCGCTCTCGCTGCTTCCTTGCGAGAGCGCTGCACTGACAGAG	600
Oy	970	CATCAGGTACCCGGCATGAGAGACCCCTTGCAGAGCTGCAGAGAGGAAGTCAAGACCA	1029
Dd	601	CATCAGGTACCCGGCATGAGAGACCCCTTGCAGAGCTGCAGAGAGGAAGTCAAGACCA	660
Oy	1030	CTTCAGGCGCTTCAAGACAGCGAGCGGGAGACACACCGAAGCGTGCAGCTCTCAAGGA	1089
Dd	661	CTTCAGGCGCTTCAAGACAGCGAGCGGGAGACACACCGAAGCGTGCAGCTCTCAAGGA	720
Oy	1090	CAACTGGGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCACTATATGGGAGGCGCTTC	1149
Dd	721	CAACTGGGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCACTATATGGGAGGCGCTTC	780

QY	1150	GAGCGGCTGCAACGGCTCTCTGCTGTAACGCCAGAAAGGCATGCTAAGAGAGCTGGAGCG	1209
Db	781	GAGCGGGCTGCAACGGCTCTCTGCTGTAACGCCAGAAAGGCATGCTAAGAGAGCTGGAGCG	840
QY	1210	GACACAGGGCCGACAGCTGACCGACATCAGACAGAAAGTCCAGAGCCTCAGCAGCACACTG	1269
Db	841	GACAGGGCCGACAGCTGACCGACATCAGACAGAAAGTCCAGAGCCTCAGCAGCACACTG	900
QY	1270	CGCAAGTCCAGAGAGGAGCCAGATCTGCAGGAGCGCTGAGTGAACCGACGGCAC	1329
Db	901	CGCAAGTCCAGAGAGGAGCCAGATCTGCAGGAGCGCTGAGTGAACCGACGGCAC	960
QY	1330	ACCTTCGTGGGTGGGGGTGGGCTCACTGTGCGAGGGGGCTCAAGGGGAAAAATCCATGAGACC	1389
Db	961	ACCTTCGTGGGTGGGGGTGGGCTCACTGTGCGAGGGGGCTCAAGGGGAAAAATCCATGAGACC	1020
QY	1390	AACCTCACATATGAAGACTTCCGCAACCTCCAAAGTACAGAGGCCCTCTGACGTACACATC	1449
Db	1021	AACCTCACATATGAAGACTTCCGCAACCTCCAAAGTACAGAGGCCCTCTGACGTACACATC	1080
QY	1450	TGGAAAGTCCCTGTTTCCAGGACATCAGCCATGCGCAGCGCCCTTAACCTTGGACCGGGC	1509
Db	1081	TGGAAAGTCCCTGTTTCCAGGACATCAGCCATGCGCAGCGCCCTTAACCTTGGACCGGGC	1140
QY	1510	ACAGCCACACAGCGCTGATCTGTGCGAGCACTGCACATTGTGGCTTACGGCAATTG	1569
Db	1141	ACAGCCACACAGCGCTGATCTGTGCGAGCACTGCACATTGTGGCTTACGGCAATTG	1200
QY	1570	CACCCACACGCACTGCAAGACTCGCCAAAGCGCTTCGATGTGAGAGTGTGGTCTGGGT	1629
Db	1201	CACCCACACGCACTGCAAGACTCGCCAAAGCGCTTCGATGTGAGAGTGTGGTCTGGGT	1260
QY	1630	TCTGAAGCGCTTCAGTAGTGGGGGTGCACACTACTGCGGAGGGTGGTGGGGGAGAAAGCCAG	1689
Db	1261	TCTGAAGCGCTTCAGTAGTGGGGGTGCACACTACTGCGGAGGGTGGTGGGGGAGAAAGCCAG	1320
QY	1690	TGGGTGATCGGGCTGCGACACAGAAAGCGCAAGCGCANAGGGCAGCATCAGATCAGACCC	1749
Db	1321	TGGGTGATCGGGCTGCGACACAGAAAGCGCAAGCGCANAGGGCAGCATCAGATCAGACCC	1380
QY	1750	AGCCGCGGCTTCTACTGCTATGCTGATGAGATGAGATGGCAACAGTACAGCGCTGACGGAG	1809
Db	1381	AGCCGCGGCTTCTACTGCTATGCTGATGAGATGAGATGGCAACAGTACAGCGCTGACGGAG	1440
QY	1810	CCCTGAGCGGGCTTAACGTCCGGAGACAAGCTTGACAAAGGTGGGTCTTCTGTGACTAT	1869
Db	1441	CCCTGAGCGGGCTTAACGTCCGGAGACAAGCTTGACAAAGGTGGGTCTTCTGTGACTAT	1500
QY	1870	GACCAAGGCTTGCATCATTCTTAACAAAGCTATGACATGTCCTGGCTCTACCTTCCGC	1929
Db	1501	GACCAAGGCTTGCATCATTCTTAACAAAGCTATGACATGTCCTGGCTCTACACCTTCCGC	1560
QY	1930	GAGAAGTTCCTTGCGCAAGCTGTGCTTACTTCAACGCTTGCGCCGACAGCCACAGCCAAATGGC	1989
Db	1561	GAGAAGTTCCTTGCGCAAGCTGTGCTTACTTCAACGCTTGCGCCGACAGCCACAGCCAAATGGC	1620
QY	1990	AAGAAGCTTCAAGCGGCTGCGGATCAACAGCGTCCGATCTTAGTCAGAGAGAGAGACC	2049
Db	1621	AAGAAGCTTCAAGCGGCTGCGGATCAACAGCGTCCGATCTTAGTCAGAGAGAGAGAGACC	1680
QY	2050	ACAACCTCTGCGGACCACTGCGCACTGCGAAGAGCGCCGACAGGAAGATAGAAAGCTGG	2109
Db	1681	ACAACCTCTGCGGACCACTGCGCACTGCGAAGAGCGCCGACAGGAAGATAGAAAGCTGG	1739
QY	2110	ACTCCAGGCCACAGCTGGGCACTGAGAGACTGAGCGCAGTTGTATTAACCTCAGAGCTCAG	2169
Db	1740	ACTCCAGGCCACAGCTGGGCACTGAGAGACTGAGCGCAGTTGTATTAACCTCAGAGCTCAG	1799
QY	2170	TCTGTAAATGAGAGTGCATTCCTCACTTCTTAACCTCTCTTCACAGCATCGATGTTCTG	2229
Db	1800	TCTGTAAATGAGAGTGCATTCCTCACTTCTTAACCTCTCTTCACAGCATCGATGTTCTG	1859

OY	2230	TAGCTCGACCTTATAGGGATPACAGCTTTGATCCAGAGATGTGACATGGCTTCTCTCA	2289
Db	1860	TAGCTCTGACCTTATAGGGATPACAGCTTTTATCCAGAGATGACAGGGCTTCTCTCA	1919
OY	2290	GGGCAACCCCTGGCCCAACCTCTATCCCATCTTCTCAGGGGCAAGGGACTACCTCCAGT	2349
Db	1920	GGGCAACCCCTGGCCCAACCTCTATCCCATCTTCTCAGGGGCAAGGGACTACCTTCCAGT	1979
OY	2350	GTCCTCCCTCAGGCCAGCCGCTGACCTCAGGAAGTGTGAGACATGGCCAGTAGTTGGCAG	2409
Db	1980	GTCCTCCCTCAGGCCAGCCGCTGACCTCAGGAAGTGTGAGACATGGCCAGTAGTTGGCAG	2039
OY	2410	CCCCAAGACACACAGCACCCCTCTTATGTCCCATAGGCTTAAGACTTACCCCTGACAAAC	2469
Db	2040	CCCCAAGAACACACAGCACCCCTCTTATGTCCCATAGGCTTAAGACTTACCCCTGACAAAC	2099
OY	2470	TAGTAGTAGGGGSCATTTTACCTCTTGACCCCAAGTCACAGAGTGACACAGGTAGTACCTGGTCC	2529
Db	2100	TAGTAGTAGGGGSCATTTTACCTCTTGACCCCAAGTCACAGAGTGACACAGGTAGTACCTGGTCC	2159
OY	2530	TAGGGTGGCTGAGAGCCAACCTCTCCTGCCACCCCAACACACAAAGTATATGTTGGTCT	2589
Db	2160	TAGGGTGGCTGAGAGCCAACCTCTCCTGCCACCCCAACACAAAGTATATGTTGGTCT	2219
OY	2590	ACTCTCTCCCATGTATCTGTGTGTGACATGTATGTCTGTGGGCTGTGCAAGCACCTGGTA	2649
Db	2220	ACTCTCTCCCATGTATCTGTGTGTGACATGTATGTCTGTGGGCTGTGCAAGCACCTGGTA	2279
OY	2650	GTTGAGTCCACACATTTATAGTCATGTGTGCACACACCTCTCTGCCACAGGGCCAGGGAGAG	2709
Db	2280	GTTGAGTCCACACATTTATAGTCATGTGTGCACACACCTCTCTGCCACAGGGCCAGGGAGAG	2339
OY	2710	GGTGAAGGATATACCCAAAGCTGTATGACAGAGCCATTAGCTTAAAGCAACTGTGACAGACAA	2769
Db	2340	GGTGAAGGATATATACCCAAAGCTGTATGAGACAGAGCCATTAGCTTAAAGCAACTGTGACAGACAA	2399
OY	2770	GCCCTCCCTGGATGATCAGAGTCCCAAGTAGTCTGTGAACAGATGCCAACCCCTCTTC	2829
Db	2400	GCCCTCCCTGGATGATGAGAGTCCCAAGTAGTCTGTGAACAGATGCCAACCCCTCTTC	2459
OY	2830	AGCCAGGCGCTGTGAGACCTGCTTAGGGGTGACAGAGGCTCCAGAAAGAGTGTGTGAATTA	2889
Db	2460	AGCCAGGCGCTGTGAGACCTGCTTAGGGGTGACAGAGGCTCCAGAAAGCAATGTGTGAATTA	2519
OY	2890	GGACCCCAAGCACTGGGAGGGGCTGTGGCTAGACCCCTTGTGCAGACTTGGCATCTATCTC	2949
Db	2520	GGACCCCAAGCACTGGGAGGGGCTGTGGCTAGACCCCTTGTGCAGACTTGGCATCTATCTC	2579
OY	2950	AGTTAGGATCTGTGCTGCGACGAAAACAGAGCCACTTGTAGCTGTGTTTAATTAGACAAGAT	3009
Db	2580	AGTTAGGATCTGTGCTGCGAGAAAACAGAGCCACTTGTAGCTGTGTTTAATTAGACAAGAT	2639
OY	3010	TTACTACCTGGCCCGCTGGGTGCTGCAAAAATGTTGGAAGAGCTGGGAAGACAGACTGTG	3069
Db	2640	TTACTACCTGGCCCGCTGGGTGCTGCAAAAATGTTGGAAGAGCTGGGAAGACAGACTGTG	2699
OY	3070	CTGAATTTCCAGGAACCTCCACGCGCAGCAATTCATCTGTCTGTTGACCCAGGAAAGCTG	3129
Db	2700	CTGAATTTCCAGGAACCTCCACGCGCAGCAATTCATCTGTCTGTTGACCCAGGAAAGCTG	2759
OY	3130	CCCCCATCTGACAGGAAGCCACTATGCCAGAAAGCTGCTGACTGCAAGACTAGGCTCCCTC	3189
Db	2760	CCCCCATCTGACAGGAAGCCACTATGCCAGAAAGCTGCTGACTGCAAGACTAGGCTCCCTC	2819
OY	3190	TGCCACGGTCTGTGCAAGCCAAATAGATGCTGTGAGGCTGTGGCCCTCTCCCACTTCACTCA	3249
Db	2820	TGCCACGGTCTGTGCAAGCCAAATAGATGCTGTGAGGCTGTGGCCCTCTCCCACTTCACTCA	2879
OY	3250	GTTCCCAATCTAAATTTTTTACAGAGATCTGTGTTGGGGACACTTAAGTCAGATCCAGA	3309
Db	2880	GTTCCCAATCTAAATTTTTTACAGAGATCTGTGTTGGGGACACTTAAGTCAGATCCAGA	2939
OY	3310	ACCTTGGCTGCAAGGAGCTGTGGGAATGTCTATTTCCCTAGAGAAAGTTAGGTTGGGTG	3369

	Db	2940	ACCTGGCGTGTGAAGGAGTCTGGGAAATGTCATCTCCCTAGAAAGATTAGGTGGCTG	2999
Oy	3370	GAGCAAGCCCCACCCTGGGTTTTTTTGCCACAGCATCCCAATCGTGAAACACTCGGGGAGG	3429	
Db	3000	GAGCAAGCCCCACCCTGGGTTTTTTTGCCACAGCATCCCAATCGTGAAACACTCGGGGAGG	3059	
Oy	3430	GTCGAGTCCACATCTAGAGGTGTCCTGCCCTTGGCTCTATACCTCGCCAGAGTGGCAA	3489	
Db	3060	GTCGAGTCCACATCTAGAGGTGTCCTGCCCTTGGCTCTATACCTCGCCAGAGTGGCAA	3119	
Oy	3490	CTGAGAGAGTGGGCTGCAGACCTAGCCTTAATGTCTCCCGGCTTGACTTTCTTCT	3549	
Db	3120	CTGAGAGAGTGGGCTGCAGACCTAGCCTTAATGTCTCCCGGCTTGACTTTCTTCT	3179	
Oy	3550	AGTCTGGGGGCTTAGATTTGTCACTTTGGGGGTCGTGACACAACACACATCCCAAGTAG	3609	
Db	3180	AGTCTGGGGGCTTAGATTTGTCACTTTGGGGGTCGTGACACAACACACATCCCAAGTAG	3239	
Oy	3610	CCGGAAGAGCTTAACACAGAGGGGTTCTTAAATAATGCTGCCCCTCCACCCGGGCTTCT	3669	
Db	3240	CCGGAAGAGCTTAACACAGAGGGGTTCTTAAATAATGCTGCCCCTCCACCCGGGCTTCT	3299	
Oy	3670	TGGGCAAAAGAATTTGTACAGCCCTAACCCCAACCTTCACTACCAATCTGGGCCACC	3729	
Db	3300	TGGGCAAAAGAATTTGTACAGCCCTAACCCCAACCTTCACTACCAAGATCTGGGCCACC	3359	
Oy	3730	CAGAGATATTTTATTTAAAAATGTGGCCATTTATGATGATGATGATGATTTGATTTAAA	3789	
Db	3360	CAGAGATATTTTATTTAAAAATGTGGCCATTTATGATGATGATGATGATTTGATTTAAA	3419	
Oy	3790	TTAAAGTTACAGATGTC 3806		
Db	3420	TTAAAGTTACAGATGTC 3436		
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LOCUS	AK001621	Homo sapiens cDNA FLJ10759 fls, clone NT2RP3004617, weakly similar		
DEFINITION	LOCUS	TO ZINC-BINDING PROTEIN A33.		
ACCESSION	AK001621	AK001621.1 GI:7022986		
KEYWORDS	KEYWORDS	oligo capping; fls (full insert sequence).		
SOURCE	SOURCE	Homo sapiens (human)		
ORGANISM	ORGANISM	Homo sapiens		
REFERENCE	REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	JOURNAL	Ishigai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,		
REFERENCE	AUTHORS	Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K.,		
TITLE	JOURNAL	Tanai,H., Kimata,M., Matanabe,M., Hirooka,S., Ishii,S., Kawai,Y.,		
COMMENT	COMMENT	Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Negahara,K., Masuhio,Y. and Kanehorai,K.		
		NEDO human cDNA sequencing project		
		Unpublished		
		2 (bases 1 to 3436)		
		Ishigai,T. and Otsuki,T.		
		Direct Submission		
		Submitted (16-FEB-2000) Takao Ishigai, Helix Research Institute,		
		Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan		
		(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3966)		
		NEDO human cDNA sequencing project supported by Ministry of		
		International Trade and Industry of Japan; cDNA full insert		
		sequencing: Research Association for Biotechnology; cDNA library		
		construction, 5'- & 3'-end one pass sequencing and clone selection:		
		Helix Research Institute (supported by Japan Key Technology Center		
		etc.) and Department of Virology, Institute of Medical Science,		
		University of Tokyo.		
FEATURES	FEATURES	Location/Qualifiers		
Source	Source	1..3436		
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		/mol_type="mRNA"		

Query Match	Similarity	Score	DB	Length
Beat Local	99.9%	Pred. No. 0;		
Matches 3433;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
0Y	370	CCACTACTCTGAGACTGGCCCTCCCGGGGCTGGCGCTCCCGACGAGTCTCAGCGCGGACCCC	429	
Db	1	CCACTACTCTGAGACTGGCCCTCCCGGGGCTGGCGCTCCCGACGAGTCTCAGCGCGGACCCC	60	
0Y	430	TTTCCTGCGGTATACCTCTCTTCGCGAGACACACCCCTCCCTCTCGCGGAGTCTTACCCC	489	
Db	61	TTTCCTGCGGTATACCTCTCTTCGCGAGACACACCCCTCCCTCTCGCGGAGTCTTACCCC	120	
0Y	490	TGCGCTGCGGGGCTGTCCTCCCGGCGCCAGCCCTCGGTGTCCTCCGACAGCGCGCGC	549	
Db	121	TGCGCTGCGGGGCTGTCCTCCCGGCGCCAGCCCTCGGTGTCCTCCGACAGCGCGCGC	180	
0Y	550	TTCTCTCAGCGCGCGCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	609	
Db	181	TTCTCTCAGCGCGCGCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240	
0Y	610	TGCAAGCTCTCAGAGAGAGAGT	669	
Db	241	TGCAAGCTCTCAGAGAGAGAGT	300	
0Y	670	AGCCTGGGCTGCGAGCACTTCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	729	
Db	301	AGCCTGGGCTGCGAGCACTTCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	360	
0Y	730	GAGGCGGAGGCG	789	
Db	361	GAGGCGGAGGCG	420	
0Y	790	GCGCGCAGGCTCTGAGT	849	
Db	421	GCGCGCAGGCTCTGAGT	480	
0Y	850	ATCTCTCAACG	909	
Db	481	ATCTCTCAACG	540	
0Y	910	TGCGCTCAGAGAGCG	969	
Db	541	TGCGCTCAGAGAGCG	600	
0Y	970	CATCAGGCTCAGCGGATCTGAGAGGCTCTGAGAGGCTCTGAGAGGCTCTGAGAGGCT	1029	
Db	601	CATCAGGCTCAGCGGATCTGAGAGGCTCTGAGAGGCTCTGAGAGGCTCTGAGAGGCT	660	

QY	1030	CTTCAGGCCCTTCAAGACAGGAGGGGGAGACACACGAAAGGGCTGCACCTGCTCAAGCGA	1089
Db	661	CTTCAGGCCCTTCAAGACAGGAGGGGGAGACACACGAAAGGGCTGCACCTGCTCAAGCGA	720
QY	1090	CAACTGGGGGAGACCMACTCTTCCACCAAGAGCTTGGGAGACCTATATGGCGAGGCTTC	1149
Db	721	CAACTGGGGGAGACCMACTCTTCCACCAAGAGGCTTGGGAGACCTATATGGCGAGGCTTC	780
QY	1150	GAGGGGCTGCACCCGCTGCTGGGTAAAGGCCAAGAGGCGATGTAGAGACTGGAGGCG	1209
Db	781	GAGGGGCTGCACCCGCTGCTGGGTAAAGGCCAAGAGGCGATGTAGAGACTGGAGGCG	840
QY	1210	GACAGGGCCCGCAGCTGACCGACATCGAGCAGAAAGTCCAGCGCTACAGCCAGACCTG	1269
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QY	1270	CGCAAGGTCCAGAGAGGAGGCCAGATCTGCAAGAGCGGCTTGCTGAACCAGCCGCGAC	1329
Db	901	CGCAAGGTCCAGAGAGGAGGCCAGATCTGCAAGAGCGGCTTGCTGAACCAGCCGCGAC	960
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 ORGANISM
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 Strausberg, R.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (11-DEC-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guln,

Leticia Hsiao, Martin Krzywinski, Reta Kutscher, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Nese, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Zetter.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LBL at: <http://image.lbl.gov>
Series: IRAL Plate: 6 Row: 3 Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022986.
Location/Qualifiers

FEATURES

SOURCE

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CDS

BASE COUNT 738 a 1021 c 858 g 642 t
ORIGIN

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 3259)
 Strausberg, R.
 Direct Submissions
 Submitted (15-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 CONTACT: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada

info@bgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Neas, Pawan Pandoh, Anna-Elisa Prabhu, Parveen Speedi, Jacqueline
Schlein, Diane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natasja Van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Zutra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILMIL at: <http://image.llnl.gov>
Series: IRAL Plate: 23 Row: a Column: 20.

FEATURES

Source

Location/Qualifiers

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BASE COUNT 738 a 1021 c 858 g 642 t
ORIGIN

Query Match 84.5%: Score 3232; DB 9; Length 3259;
Best Local Similarity 99.9%: Pred. No. 0;

Matches 3254; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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DEFINITION			
BC012152			
ACCESSION			
BC012152.1 GI:15082475			
VERSION			
MGC.			
KEYWORDS			
Homo sapiens (human)			
SOURCE			
Homo sapiens			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
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1 (bases 1 to 3259)			
AUTHORS			
Strausberg, R.			
TITLE			
Direct Submission			
JOURNAL			
Submitted (02-AUG-2001) National Institutes of Health, Mammalian			
Gene Collection (MGC), Cancer Genomics Office, National Cancer			
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
USA			
REMARK			
COMMENT			
NIH-MGC Project URL: http://mgc.ncl.nih.gov			
Contact: MGC help desk			
Email: cgapsb-r@mail.nih.gov			
Tissue Procurement: ATCC			
CDNA Library Preparation: Rubin Laboratory			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)			
DNA Sequencing by: Genome Sequence Centre,			
BC Cancer Agency, Vancouver, BC, Canada			

info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutache, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Scheln, Diane Smajlus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNU at: <http://image.llnl.gov>
Series: IRL Plate: 29 Row: d Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES
Source

Location/Qualifiers
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CDS

BASE COUNT

738 a 1021 c 858 g 642 t
ORIGIN

Query Match 84.5% Score 3232; DB 9; Length 3259;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 2; Gaps 2;
Matches 3254; Conservative 0; TmMatches 0; Indels 2; Gaps 2;

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OY	2191	TCCCTACTTCTTAACTCTTCCAGCATGATGTTCTGTAGCTGTACCTGTATAGGA	2250	OY	3271	CAAGATTTCTGTTTGGGGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCT	3330
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OY	2251	TACAGTTGATCCAAAGATGTGACATGCGCTCTCTCAGGGCAACCCCTGCCAACCT	2310	OY	3331	GGGAAATGTCATTTCCTAGAGAAAGTTAAGGTGGGTGGAGCAAGCCCACTGCGTTT	3390
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REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: ARCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mcgenhr@nisc.nih.gov

Shvachko, Y., Wetherby, K.D., Bouffard, G.G., Brinkley, C., Brooks, S.,
Benjamin, B., Blakeley, R.W., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Statilipop, S., Thomas, P.J.,
Tongson, E.E., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/BLM at: <http://image.llnl.gov>
Series: IMAL Plate: 27 Row: b Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES

Source

Location/Qualifiers

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CDS

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ORIGIN

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VERSION AX491283.1 GI:22323984
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Killary,A., Chandler,D. and Lott,S.
TITLE The tumor suppressor car-1
JOURNAL Patent: WO 0212285-A 7 14-FEB-2002;
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OY	3229	GCCCCCTGCCACTTCACTCAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCAAAAT	3288			
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OY	3349	AGAAAGAACTTATGAGTGGTGGAGCAAGCCCACTGCTGTTTCTGCAAGCATCCAA	3408			
DB	14399	AGAAAGAACTTATGAGTGGTGGAGCAAGCCCACTGCTGTTTCTGCAAGCATCCAA	14458			
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DB	14459	TGCTGAAGAACTCGGAGAGGGGTGAGTCCACATCTAGGGTTCCTGCCCTTGCTCT	14518			
OY	3469	ATCCCTGCGCAGAGGTGGGAACTGAGAGAGTGGGTGCAAAACATGAGCTTAAATGTCTC	3528			
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QY 2029 TAGTCAGGCGAAGAGAGACCAACACCTCTGGGACCACTGCGACACTGCAAGAGCCCTGC 2088
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 Db 19111 TAGTCAGGCGAAGAGAGACCAACACCTCTGGGACCACTGCGACACTGCAAGAGCCCTGC 19052
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 Db 18872 ATGTGACATGGCTCTCTCTGAGGGAACCCCTGGCCAAACCTTCATCCCATCTCTCAGG 18813
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 Db 18812 GGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGAGAGTGTGAG 18753
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 Db 18752 AGCATGGCCAGTACTTGGCAGCCCGAAAGACACACAGACCCCTCTTATGTCCCATGSCCT 18693
 QY 2449 AAGACTTACCCCTGACCAAGCTAGTGAATGGGCACTTTAACCTTGACCCCACTCCACAGTG 2508
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 Db 18692 AAGACTTACCCCTGACCAAGCTAGTGAATGGGCACTTTAACCTTGACCCCACTCCACAGTG 18633
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 DEFINITION sequence.
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 VERSION AL662907.11 GI:21531085
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 64693)
 AUTHORS Van Heilmond, Z.
 TITLE Direct Submission
 JOURNAL Submitted (18-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, Ch10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk; clone requests: clones@sanger.ac.uk
 On Jun 21, 2002 this sequence version replaced gi:20145349.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with

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VERSION	AX491284.1	GI:22323985	
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Killary,A., Chandler,D. and Lott,S.		
TITLE	The tumor suppressor car-1		
JOURNAL	Patent: WO 0212285-A 8 14-FEB-2002;		
FEATURES	BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)		
source	I. .30676		

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Best Local Similarity	98.7%	Pred. No. 0									
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OY	1429	GGCCCCCTGCAGTACACCAATCTGGAAATGCCCTTTCACAGACATCCACCCAGTGCAGCC	1488								
DB	23371	GGTCCACAGAGCTTCTCCCACTCATCTTCTCTCCCTCCCTCCACACCCCAAGTGCAGCC	23430								
OY	1489	GGCCCTAACCCCTGGAGCCCGGGGACACAGCCACACAGCGCTCATCTCTCTGGACAGCTGCACC	1548								
DB	23431	GGCCCTAACCCCTGGAGCCCGGGGACACAGCCCAACAGCGCTCATCTCTCTGGACAGCTGCACC	23490								
OY	1549	ATTGTGGCTTACGGCACTTGCACCCACAGCCACTGACAGACTCGCCAAAGCGCTTCGAT	1608								
DB	23491	ATTGTGGCTTACGGCACTTGCACCCACAGCCACTGACAGACTCGCCAAAGCGCTTCGAT	23550								
OY	1609	GTGAGAGTGTGCGTGCTGGGTTCTGAAGCCTTACGATAGTGGGTCCTACTACTGGAGTG	1668								
DB	23551	GTGAGAGTGTGCGTGCTGGGTTCTGAAGCCTTACGATAGTGGGTCCTACTACTGGAGTG	23610								
OY	1669	GTGTGTGCGGAGAAAGACCCAGTGGGTGATGGGCTGGACACAGAACCCCAAGCCGCAAG	1728								
DB	23611	GTGTGTGCGGAGAAAGACCCAGTGGGTGATGGGCTGGACACAGAACCCCAAGCCGCAAG	23669								
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DB	23670	GGCAGCATCCAGATCCAGCCCAAGCCGCGCGTTTACTGCATGATGCACGATGGCAAC	23729								
OY	1789	CAGTACAGACGCGCTGCACAGGACCCCTGGACGCGCTTACGTCGCGGAGACAGCTTGACAAG	1848								
DB	23730	CAGTACAGACGCGCTGCACAGGACCCCTGGACGCGCTTACGTCGCGGAGACAGCTTGACAAG	23789								
OY	1849	GTGGGTGTCTTCTTGACATATGACCAAGGCTTCTCATCTTCTACAACTGATGACATG	1908								
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OY	2329	GGCAGGGGACTACCTTCCAGTGTCTCTCCCTCAGCCCAAGCCCTGACCTCAAGAAATGTCTAG	2388								
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RESULT 12
AF161326
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Center: Institute of Molecular Biotechnology
Center code: IMB
Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de

----- Project Information -----
Center project name: H176
Center clone name: CTA-392H5

----- Summary Statistics -----
Sequencing vector: M13; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 122353 bases at least Q40
Consensus quality: 127794 bases at least Q30
Consensus quality: 131293 bases at least Q20
Quality coverage: 5.82 x in Q20 bases; sum-of-contrigs

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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality 10.
Quality levels above 40 are expected to have less than

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[illegible]

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OY		3707	AACATACAGAAATCTGGGGCACCCGACAGATTTTATTTTAAAATGTGGCCATTTATG	3766
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OY		3767	AGTTATGATCAATTTGTATTAAATTTAAAGTTACAGATGTCA	3807
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1									
AUTHORS	Killary,A., Chandler,D. and Lott,S.									
TITLE	The tumor suppressor car-1									
JOURNAL	Patient: MO 0212285-A 5 14-FEB-2002;									
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QY	1429	GGCCCCCTGCAGTACACATCTGGAAGTCCCTGTCCAGAGACATCCACCCAGTGGCCAGCC	1488							
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QY	1729	GGCAGCATTCAGATTCAGGCCACGCGGGGTTTACTGATCGTGTGATGGACATGGGCAAC	1788							
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 VERSION BC049095.1 GI:29294764
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 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE 1 (bases 1 to 3216)
 AUTHORS Struhsberg, R.L., Felngold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Shanmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buelow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hele, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Kana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McKwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulys, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalske, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Morris, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 3216)

AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2003) National Institutes of Health, Mammalian

REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT	Contact: MGC help desk

Web site: <http://genome.utowa.edu>
Contact: benito-soares@utowa.edu; tom-casaavant@utowa.edu
Bonaldi, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
Fisher, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Scheffer, K.,
Schaez, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J.,
Casaavant, T., Soares, M.B.

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
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OY	1054	CGGGAAACACCCGAAAGCGCTCAGCTGCTCAAGCGACAACTGGCGGAGACCAAGTCTTCC	1113
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OY	1294	ATCCCTCGAGGAGCGGCTGGCTGAAGAACCAACCCGGGACACCTTCTGAGGTGGGCTG	1353
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OY	1354	CTGTCCGAGCGGCTTCAGAGGAAAAATCATGAGACCAACTCATATGAAAGACTTCCCG	1413
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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Killary,A., Chandler,D. and Lott,S.
TITLE       The tumor suppressor car-1
JOURNAL     Patent: WO 0212285-A 6 14-FEB-2002;
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DB      24524 TTGAGTGGCCATACCTCTAGACTGCGCCCGGGGCTGGGCTCCACGGAGTCTCAGCC 24583

QY      421 GCGCACCCCTTCTCGCTTACCTCTCCGAGACAGACCCCTCCCTCTCCGGTAGC 480
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DB      24823 GACCCGGTGAAGCTGGGCTGCGAGACACTTCTGCCGCGCTGATCAGGAGACTGG 24882

QY      721 GTGCGGCAAGAGGCGAGGGGCGCGGAGTGGCCCGAGTGGCGGCGAGCTTCCGAG 780
      |||
DB      24883 GTGCGGCAAGAGGCGAGGGGCGCGGAGTGGCCCGAGTGGCGGCGAGCTTCCGAG 24942

```

```

QY      781 CCCGCGCTGGCGCCCGACCTTCAAGCTGGCCAAATCTGTGAGCGCTACAGCTCTTCCG 840
      |||
DB      24943 CCCGCGCTGGCGCCCGACCTTCAAGCTGGCCAAATCTGTGAGCGCTTACAGCTCTTCCG 25002

QY      841 CTGAGCCCAATCTCAAGCGCGCGCGCGCGCGGACCTTGCAGGCGCACAGAGATC 900
      |||
DB      25003 CTGAGCCCAATCTCAAGCGCGCGCGCGCGCGGACCTTGCAGGCGCACAGAGATC 25062

QY      901 AAGCTTTCGCTCAGGAGCGCGGCTTCTGCTTCTTCTGCGAGAGCGCTGACAGT 960
      |||
DB      25063 AAGCTTTCGCTCAGGAGCGCGGCTTCTGCTTCTTCTGCGAGAGCGCTGACAGT 25122

QY      961 CACGAGCAGATCAGGTACCGGCAATCAGAGACGCTTGCAGAGAGTGCAG 1011
      |||
DB      25123 CACGAGCAGATCAGGTACCGGCAATCAGAGACGCTTGCAGAGAGTGCAG 25173

```

Search completed: October 8, 2003, 19:06:06
Job time : 13603 secs

THIS PAGE BLANK (USPTO)

Query Match 2.88; Score 106; DB 2; Length 3416;
 Best Local Similarity 53.88; Pred. No. 7.8e-14;
 Matches 242; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

1482 GCGAGCGCCCTACCCCTGGAGCCGGGACAGCCGACAGCCGCTGATCCCTGTGGAGCA 1541
 1373 GCTGCGGATGTGATTTTGATCCAAAACAGAACCCCATCTCTCTGTTCTGAGCA 1432
 1542 CTGCACCATTTGTGCTTACGGCACTTGCAACCCAGCACTGCAAGACTGCCAAAGCG 1601
 1433 CCAGAGAGATGTGAGGGGTGCCAA---GAGGCCCAAGATGTGCAAGAACCCCTGAGAG 1489
 1602 CTTCGATGTGAGAGTGTGCGTCTGGGTTCTGAAGCCTTCAATGATGGCGCTCACTAGT 1661
 1490 ATTTAATGTGCATTTATTTGTCTTCTGCGCTGTGAGAGCTTCAATACAGGAGACATTTACTG 1549
 1662 GGAAGTGTGTGGGAGAGAACCCAGTGGGTGATGGGGCTGACACAGAACGCCGCAAG 1721
 1550 GGAAGTGTGAGTAAAGGACAGAGAGAGAGTGAATATGAGGGGTGACAGTAAGATGTGCA 1609
 1722 CCGCAAGGAGAGCATTCAGATCCAGCCAGCCGCGCTTCTACTGATCGATGACAGA 1781
 1610 GAGAAAGGCTGGGTCAAAATGACACCTGAGAAATGTGAGATTTGGGGCTGAGACTGA 1669
 1782 TGGCAACCATGACAGCCCTGACAGAGCCCTGAGCGGGCTTAACGTCGGGACAAAGCT 1841
 1670 TGGGAATATGATATCGGACTCTACTGAGCCAGAACCAACCTGAACCTTCTTAAGCCCC 1729
 1842 TGACAAAGTGGGTGTCTTCCGAGCATATGACCAAGGCTGCTCATCTTCTACATGCTGA 1901
 1730 TAAAGAAATGGGGGTCTTCTCGAGCATATGAGACTGAGATATTCATTTCAATAGCTGT 1789
 1902 TGACATGTCTGTGCTTCTACACCTTCGCGCA 1931
 1790 GGATGATCGCATATTCATCTTCTCTGGA 1819

Db 1790 GGATGATCGCATATTCATCTTCTCTGGA 1819

Query 1902 TGACATGTCTGTGCTTCTACACCTTCGCGCA 1931
 1790 GGATGATCGCATATTCATCTTCTCTGGA 1819

RESULT 2
 US-09-220-132-158
 ; Sequence 158, Application US/09220132
 ; Patent No. 6506607
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
 ; FILE REFERENCE: 07334-074001
 ; CURRENT APPLICATION NUMBER: US/09/220,132
 ; CURRENT FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 60/079,303
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: US 60/068,821
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 158
 ; LENGTH: 1782
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-220-132-158

Query Match 2.58; Score 95.8; DB 4; Length 1782;
 Best Local Similarity 52.68; Pred. No. 1.1e-11;
 Matches 233; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

1484 GAGCGGCGCTAACCGCTGAGCCGGGACAGCCAGCCAGCGCTGATCGTGGAGCACT 1543
 1178 CAGTGACGCTGACTCTGAGACACAGCGGCTTACCCAGCTGATCTCTGTGATATC 1237
 1544 GCACCATTTGTGTGAGCACTTGCACCAAGCAGCACTGACAGACTGCGCAAGCGCT 1603
 1238 TGGCGCAAGTGTGCGTACAGTTAC---CTCCAAAGAGACCTGCGTGAACAACCCGAGAGGT 1294

1604 TCGATGTGAGAGTGTGCTGCTGGCTTCTGAAGCCTTCAGATGATGAGCCCTCAGTACTGGG 1663
 1295 TCAATCTGTTTCCCTGATGTCTTGGGCTCTCCATGCTTCATCGCGGAGACATTAATGGG 1354
 1664 AGGTGTGTGTGGGAGAGAACCCAGATGGGTGATCGGGCTGGCACAGAACCCCAAGCC 1723
 1355 AGGTAGAGGTGGAGATTAAGCCAAATGAGACCAATAGGTGTGTGGAAGACTCACTGTGCA 1414
 1724 GCAAGGCGAGCATCCAGATCCAGCCAGCCGCGCTTCTACTGATCGTATGACAGCATG 1783
 1415 GAAAGGTGGAGTAACTCAACCTCAGCCCCAGATGATTTCTGGCAGTGTCTTGTGATATG 1474
 1784 GCAACCACTACAGCGCTTGCACAGAGCCCTGAGACGCGGCTTAACGTCGGGACAAAGCTTG 1843
 1475 GAAAGATATATTGGGCTCTTCTACTCCCAATGATGCTGCTGAGGTCTCTTCAACAGCTGACAG 1594
 1844 ACAAGTGGGTGTCTCTCTGAGCATATGACCAAGGCTGCTCATCTTCTACAAATGCTATG 1903
 1355 AGCGGTGGGATTTCTTGGACTATGATGCTGTGAGGTCTCTTCAACAGCTGACAG 1594
 1904 ACATGTCTGCTGCTTACACCTTC 1926
 1595 AGAGGTGACACCTTCACTTTC 1617

Db 1595 AGAGGTGACACCTTCACTTTC 1617

Query 1904 ACATGTCTGCTGCTTACACCTTC 1926
 1595 AGAGGTGACACCTTCACTTTC 1617

RESULT 3
 US-08-232-463-14
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7218 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: pTZgpt-F15
 ; US-08-232-463-14

Query Match 2.5%; Score 94; DB 1; Length 7218;
Best Local Similarity 2.6%; Pred. No. 4e-11;
Matches 10; Conservative 257; Mismatches 117; Indels 0; Gaps 0;

```

QY 213 GGGATTCGACCCCTTAAGGCTCCACCCGCGGATGCCCTTCGCCAGCTCCTA 272
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1056 GAGCTGCGCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 273 TCCCTTAGGACGTCGCCGCCCTTAGACCTCCCGTCAGATCCTGCTCCAGCCG 332
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1116 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1175
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 333 TCCAGCTCTCTCCAGCCGCTTCCGCTTCCAGCTCTTCCAGCTCTTCCAGCT 392
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1176 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1235
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 393 CGGCTGCGGCTCCAGGAGTCTCAGCGCGGCGGCTTCCGCTTCCAGCTCTCCG 452
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1236 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1295
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 453 GACGACGACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 512
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1296 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1355
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 513 CGGCTGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 572
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1356 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1415
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 573 TCGGCGGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 596
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1416 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1439
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 4

```

US-08-724-394A-13
: Sequence 13, Application US/08724394A
: Patent No. 5872237
: GENERAL INFORMATION:
: APPLICANT: Feder, John N.
: APPLICANT: Kironmal, Gregory S.
: APPLICANT: Laufer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolff, Roger K.
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
: TITLE OF INVENTION: Sequences and Antibodies Thereo
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724, 394A
: FILING DATE: 01-OCT-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitts, Renee A.
: REGISTRATION NUMBER: 35,136
: REFERENCE/DOCKET NUMBER: 017957-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
: INFORMATION FOR SEQ ID NO: 13:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 2926 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
NAME/KEY: misc_feature
LOCATION: 1..2926
OTHER INFORMATION: /note="cDNA 29"

Query Match 2.3%; Score 86.4; DB 2; Length 2926;
Best Local Similarity 52.7%; Pred. No. 1.4e-09;
Matches 236; Conservative 0; Mismatches 206; Indels 6; Gaps 2;

```

QY 1483 CCAGCCGCTTACCTTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1542
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1186 CTTGCGGATGTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1245
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1543 TGCACCATTTGCTTACGCACTTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1602
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1246 CAGAGGAGTGTG--CAGGCTGCTGAAGAGCCGCGGAGTCTGCGAGCAACCTGAGAGA 1302
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1603 TTTGATGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1662
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1303 TTTGATGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1362
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1663 GAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1719
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1363 GAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1720 AGCCGCAAGGCGAGCATTCAGATCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1779
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1423 AGGAAAAAGTGTGGGTCAGAAATGACACCGGAGAGAGATCTGAGATAGGAGCTGAGCT 1482
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1780 GATGCAACCATGATACAGCCGCTTCCAGGAGCCCTGAGCGGCTTAAAGTCCGGAACAG 1839
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1483 GATGCAACCATGATACAGCCGCTTCCAGGAGCCCTGAGCGGCTTAAAGTCCGGAACAG 1542
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1840 CTTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1543 CTTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1602
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1900 GATGCAACCATGATACAGCCGCTTCCAGGAGCCCTGAGCGGCTTAAAGTCCGGAACAG 1927
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1603 ACAGATGATCTCATATCTACACCTTTC 1630
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 5

```

US-08-724-394A-16
: Sequence 16, Application US/08724394A
: Patent No. 5872237
: GENERAL INFORMATION:
: APPLICANT: Feder, John N.
: APPLICANT: Kironmal, Gregory S.
: APPLICANT: Laufer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolff, Roger K.
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
: TITLE OF INVENTION: Sequences and Antibodies Thereo
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724.394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3502 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..3502
OTHER INFORMATION: /note="cDNA 32"
US-08-724-394A-16

Query Match 2.2%; Score 82.8; DB 2; Length 3502;
Best Local Similarity 52.2%; Pred. No. 8.8e-09;
Matches 233; Conservative 0; Mismatches 207; Indels 6; Gaps 2;

QY 1484 CAGCCGCCCTTAACCTGGACCCGGGACAGCCACAGCCGCTGATCTGTGGAGCACT 1543
DB 1063 CTGCTGATGTGTCTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1122
QY 1544 GCACCATGTGGCTTACGGCACTTGACCACTGACCACTGACCACTGACCACTGACCACT 1603
DB 1123 GGAGAGTGTGAGGCGGGGCCCCCT--ACAGCAGAGAGTGTCTGACACCCAGAGANT 1179
QY 1604 TCGATGTGAGGTGTCTGCTGTGGTGTGAGAGCTTCACTAGTATGCGCTCCACTACTGG 1663
DB 1180 TCGACAGTCAACCTGTGTCTGATGGAGTGGAGAGTGTGCGCTCAAGGAAACATTAATG 1239
QY 1664 AGGTGTGTGTGGCGGAGAAAGACAGCTGGTGTGATGCGGCTGGACACAGAGCCGCA 1723
DB 1240 AGGTGTGTGTGGGAAACCTGTATGTGTGTGACTGTGGGGGTGTGACAGACAGTGTG 1299
QY 1724 GCAAGGGGAGATCCAGATCCAGATCCAGCCAGCGGGGCTTACTGATCGATCGATGAG 1783
DB 1300 GGAAAGGGAGAGTCTCTGATTCCTCAAAATGCTTGTGACCTGAGAGATG--TTTG 1356
QY 1784 GCAACCACTACAGCCCTGACAGAGAGCCCTGACAGCGGCTTAACGTCCGGGACAACTTG 1843
DB 1357 GAACCAATACCGGGGCGCTGTCTGATTCCTCAAAATGCTTGTGACCTGAGAGATG--TTTG 1416
QY 1844 ACAAGGTGGTGTCTCTGATGACTATGACCAAGCTTCTACTCTTCAATGCTGATG 1903
DB 1417 GCCGGGTGGGCTTCTCTGATGACTATGAGCTGTGAGATGCTCTTCAACATGAGGG 1476
QY 1904 ACATGTCTGGCTTACACCTTCCGC 1929
DB 1477 ACAGTCAACATCTACACATGTCCC 1502

RESULT 6
US-08-658-136-2
Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D

APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/658.136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 2.1%; Score 81.6; DB 3; Length 5356;
Best Local Similarity 50.6%; Pred. No. 3.8e-08;
Matches 251; Conservative 0; Mismatches 239; Indels 6; Gaps 2;

QY 101 CACCCCTCTCTCTCTGCGGGTCAAGCAATGAGCGCTGGCGCTGCGCCCTCC 160
DB 3507 CTCCCTCTCTCCACCCCT 35138
QY 161 CCCAGATTCCTCCATCCAGCTTCTGCGCTCTCCCGACCGCCCAACCCGGGATTC 220
DB 3519 TCTCTTCCCT 35198
QY 221 GACCCCTTAAGGCTCCACCCCGCTCGGGATCCCTTCTCTCCAGCTCTATCCCTTAG 280
DB 3519 TCTCTCTATCCCT 35254
QY 281 GACTCGCCGGGCGCTTAAGCTCTCGGATCCCGATCCCGCTCCAGCGCTCTACAGCC 340
DB 3525 TCT 35314
QY 341 TCTCTCCAGCGCCATTCCTTGAAGTCCCACTACTGAGAGCTCTCCGGGCTGG 400
DB 3531 TCT 35374
QY 401 GCTCCAGGAGTCTCAAGCCCGGACCCCTTCTCTGCTTACCTCTCTCCGGAGAGAG 460
DB 3537 CCTCC--TCT 35432
QY 461 CCCCCT 520
DB 3543 TCT 35492
QY 521 CCTCGGTCTGCT 580
DB 3549 CCTCCCT 35552

Qy	581	CCCTCTCTGCTGCCCC	596
Db	35553	CTCCCCCTCTTCTCC	35568

RESULT 7

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US-08-658-136-1
Sequence 16, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

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Query Match	2.1%;	Score 81.6;	DB 3;	Length 53577;
Best Local Similarity	50.6%;	Pred. No. 3.8e-08;		
Matches 251;	Conservative 0;	Mismatches 239;	Indels 6;	Gaps 2

[illegible][illegible]

RESULT 8

```

US-09-128-153-16
? Sequence 16, Application US/09128155
? Patent No. 6117654
? GENERAL INFORMATION:
? APPLICANT: Pan, Yang
? TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
? TITLE OF INVENTION: AND USES THEREOF
? FILE REFERENCE: 09404/052001
? CURRENT APPLICATION NUMBER: US/09/128.155
? CURRENT FILING DATE: 1998-08-03
? EARLIER APPLICATION NUMBER: US 60/091,650
? EARLIER FILING DATE: 1998-07-02
? EARLIER APPLICATION NUMBER: US 60/054,646
? EARLIER FILING DATE: 1997-08-04
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 16
? LENGTH: 152331
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(152331)
? OTHER INFORMATION: n = A,T,C or G
US-09-128-153-16

```

Query Match	2.1%;	Score 80.4;	DB 3;	length 152331;
Best Local Similarity	49.9%;	Pred. No. 9.5e-08;		
Matches 201; Conservative	0;	Mismatches 202;	Indels 0;	Gaps 0;

[illegible]

QY 530 TGCCTCCGACAGCGCGCGCTCTCTACGCCGCCCCCCTGGCCC 572
| | | | | | | | | | | | | | |
Db 22242 GCGCGCCGCCCAACCCCCCCCCCAAGCCCCGCCCCCGCCC 22284

RESULT 9

```

US-09-249-585A-4
? Sequence 4, Application US/09249585A
? Patent No. 6417002
? GENERAL INFORMATION:
? APPLICANT: Horlick, Robert
? TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
? FILE REFERENCE: 0867/09005
? CURRENT APPLICATION NUMBER: US/09/249,585A
? CURRENT FILING DATE: 1999-02-11
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 4
? LENGTH: 1926
? TYPE: DNA
? ORGANISM: Epstein Barr Virus
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(1926)
? OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

```

Query Match	2.08;	Score 76.2;	DB 4;	Length 1926;
Best Local Similarity	44.48;	Pred	NC	3e-07.

Matches 350; Conservative 0; Mismatches 438; Indels 1; Gaps 1,

OY		176	CCCCAGCTTTCGCGCCCTCCGGCACACGGGCCACCACCCGGGAATTTCGACCCCCTTAAGGGC	235
Db		287	CTCCCGGTCTCTGCATCCCGGTCTGTCTCTCCCGGTCTGTCTCTCTCTCTCTCTCTCTCTCTCT	346
OY		236	TCCACCCCGCTCCGGGATCCCTTTCTCCAGCTCTATCCCTTAGAGACTGCCCGGCCCC	295
Db		347	CTCCCGCTCTCCCGGTCTCCCGGTCTCCCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	406
OY		296	TAGAACCCTCCCGCGAGAGATCTCCGTCC-CGTACCCCGCTTACAGCTCTCTCTCCAGCGCC	354
Db		407	GTCCTCCCGGTCTCTCCCGGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	466
OY		355	ATCGCCTTGAGCTGCGCACTACTCTTAGACAGCCCTCCCGGGCTGGCGCTCCACAGAGTC	414
Db		467	CCGTCCTCTGCTCTCTCCCGGTCT	526
OY		415	TGACCGCGACCCCTTCT	474
Db		527	CTGCT	586
OY		475	GGTAGCTCTAACCCCTGCTGTGGGGGCTCTGTCCTCCCGGCGCACGCCCTGGGTCTGTGCT	534
Db		587	GTCCTGTCT	646
OY		535	CAGACAGCGCGGCT	594
Db		647	CTCCCGGTCT	706
OY		595	CTGGGGCATGCGCTGACGCTCTAGAGAGAGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT	654
Db		707	CTGCT	766
OY		655	TACACAGACCCGGGTGAGACCTGGGGCTGGAGACACTTCTGGCGCGCTGATCAGAGAG	714
Db		767	CTCCCGGTCT	826
OY		715	CACCTGGGTGGGACAGAGAGCGCACAGCGGCCCGGACTGCCCCGAGTGCACGGCGCACAGTTT	774
Db		827	CTCCCGGTCT	886
OY		775	GCCGAGCCGGCGCTGGCGGCCACGCTTCAAGCTGGCCACAATCTGGAGCGCTACAGCTTC	834

[illegible]

RESULT 10

```

US-09-130-114-2
? Sequence 2, Application US/09130114
? Patent No. 5976807
? GENERAL INFORMATION:
? APPLICANT: Horlick, Robert A.
? APPLICANT: Damaji, Bassam B.
? APPLICANT: Robbins, Alan K.
? TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
? TITLE OF INVENTION: From Multiple Transfected Episomes
? FILE REFERENCE: 0867/1090301
? CURRENT APPLICATION NUMBER: US/09/130,114
? NUMBER OF SEQ. ID NOS.: 36
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ. ID NO. 2
? LENGTH: 1931
? TYPE: DNA
? ORGANISM: EBNA
US-09-130-114-2

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Query Match	Score	DB 2;	Length
2.08;	76.2;	1931	

Matches 350; Conservative 0; Mismatches 438; Indels 1; Gaps 1;

176	CCCAAGCTTCAGCCCTCCCGACACGCCCCACCCGGGATTTTCAGCCCTTAAAGGC	235
Db		
287	CTCCCCGTCTGTCTCCCGCTCGTCTCGTCTCCGCCGTCGTCCTCCCGTTC	346
OY		
236	TCCACCCGCTCCGGGATCCCTTCTGCCAGCTCTATCCCTTAGAGACTGCCCCCCC	295
Db		
347	CTCCCGTCTCTCCCGTCTCCCGTCTCGTCTCTCCCGTCTCGTCTCTCTCC	406
OY		
296	TAGAACCTCCCGTGAAGATCTCCGTCC-CTCAGCGGCTCAGACCTCTCCAGCGCC	354
Db		
407	GTCCTCCCGTCTCCCGTCTCCGTCCTCGTCTCCGCCGTCGTCGTCCTCCCGTCTC	466
OY		
355	ATCGGCTTAGTGGCCACTACCTCTAATCTAGTCCCTCCCGGGCTGGGGTCCAGGATC	414
Db		
467	CCCGTCTGTCTCTCTCCCGTCTCCCGTCTCTCCCGTCTCTCGTCTCTCTCCGTC	526
OY		
415	TGAGCCGCGCACCCCTTCCTGCGTTTACCTCTTTCGCGAGCAGCACCCCTCCCTTCC	474
Db		
527	CTGTCTCTCTCTCCCGTCTCCCGTCTCTCTCTCTCTCTCCCGTCTCTCCCGTCTCC	586
OY		
475	GGTAGCTCTAACCCCTGCGCTGTGGGGGCGCTGCCCGCGCACGCCCTGGGTGCTCT	534
Db		
587	GTCCTGTCTCTCTCCCGTCTCTGCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTGTC	646
OY		
535	CCGACAGCGCGCGCTCTCTCAGCGGCCCTCCCGTCCGGGCCCCCTCTGTGTGCC	594
Db		
647	CTCCCGTCTCTCTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTGTC	706
OY		
595	CCTGGCGGCATGGCGGTGAGCTCTCAAGACAGAGTCTGTGTCTCATCTCGCTGAGATC	654
Db		
707	CTGTCTCTCCCGTCTCTCTCTCCCGTCTCTGCTCTCTCCCGTCTCTCCCGTCTCTGTC	766

OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-13

Query Match 1.9%; Score 73; DB 3; Length 320;
Best Local Similarity 52.1%; Pred. No. 5.6e-07;
Matches 163; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

```

QY 155 CCGTCGCCAGAGTTCCTCCATCCCAAGCTTCGCGCTCCCGGACCGCCCGCCCGG 214
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 313 CCGTCGTCACAGTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 215 GATTTCGACCCCTTAAGGGCTCCAGCCCGGCTCGGGAGTCCCTTCGCCAGCTGATTC 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 253 CCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 275 CTTAGAGACTGCCCGCCCGCCCTAGAACCTCCCGTACAGATTCGCTCCCTACGCGCTC 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 193 CCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 335 ACAGCTCTCTCCAGCGCCCATCGCTTGAGCTGCCCATCTCTACAGCTGCGCTCCG 394
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 133 CCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 395 GCGTGGCGTCCACAGAGTCTCAGCGCGGACCGCCCTTCGCGGTTACGCTTCGCGGA 454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 73 CCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 14
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 455 CAGCAGCCCGCTCC 467
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 13 CCGCCCGCCCGCCCG 1
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 14

US-08-724-394A-12
Sequence 12, Application US/08724394A
Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fiteb, Renee A.
REGISTRATION NUMBER: 35,136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2882 base pairs

TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..2882
OTHER INFORMATION: /note= "cDNA 21"

Query Match 1.9%; Score 73; DB 2; Length 2882;
Best Local Similarity 51.3%; Pred. No. 1.1e-06;
Matches 225; Conservative 0; Mismatches 205; Indels 9; Gaps 2;

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QY 1497 CCGGACCCGGGACAGCCACGACGCTGATCTGTGCGAGACTGACCATTTGGC 1556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1203 CCGTGCATCAGACACCGCTCATCCGATCTCTCTGTACAGAGACGGAGAGTGTAG 1262
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1557 TTACGGCACTTGCACCCAC-----AGCCACTGCAGACTGCGCAAGCCCTTCGATGT 1610
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1263 AAGTGCCCTTCAGGCACTAGGGAGAGCGTGCTGTACAAACCCAGAGATTGACAG 1322
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1611 GGAGGTGCGGTGGTGGTGTGAGAGCTTCAGTAGTGGCGTCCACTGAGGAGTGGT 1670
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1323 TCAGCTTGTGTCTTAGCCCGGAGAGCTTTCCTTCAGGAAACATTACTGGAGGTGA 1382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1671 GGTGGCGGAGAAACAGGAGGAGTGTGAGCTGTGACACGAAAGCCGACCGCAAGG 1730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1383 GGTGAAACGATGATGTAGTGTGAGTGTGGGGTGTGTAGACAGTGTGAGAGAAAG 1442
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1731 CAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGCATCTGTGATGACAGATGCAACCA 1790
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1443 GGAGGTCTGTGATCTCTCAGAAATGCTTGTGACCTTGGAGATGCTAAAG--GCA 1499
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1791 GTACAGCCCTGACAGGAGCCCTGAGCGGCTTAACGTCGCGGACAAAGTTGACAAAGT 1850
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1500 ATACCGGGCGCTGTCTCTCCCGCTGATGAGATCTCTCCCTTGAAGAGTCCCTTTCGGG 1559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1851 GGGTGTCTTCTGTGATGACCAAGGCTTGTCTGATCTTACAAATGCTGATGACATGTC 1910
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1560 GGGCGCTTCTGTGATGAGTGTGAGATGTCTCTTACAAATGAGGAGACAGATC 1619
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1911 CTGCTCTACACCTTCCG 1929
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1620 GCACATCTACACATGTCC 1638
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 15

US-09-165-264-11/C
Sequence 11, Application US/09165264
Patent No. 6197510

GENERAL INFORMATION:
APPLICANT: Vinayagamorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 11
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11

Query Match 1.9%; Score 72.8; DB 3; Length 320;
Best Local Similarity 51.9%; Pred. No. 6.2e-07;
Matches 164; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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QY 270 CTATCCCTTAGAGTCCCGCCCGCCCTTGAACCTCCCGTACGATCTCCCTCAGC 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 14:53:52 ; Search time 948 Seconds
(without alignments)
10894.567 Million cell updates/sec

Title: US-09-927-091-3

Perfect score: 3826
Sequence: 1 agcctgcgtgcgcgaagc.....aaaaaaaaaaaaaaaaaa 3826

Scoring table: IDENTITY_NDC
Gap 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: /SIDSI/gcgdata/geneseq/emb1/NA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/emb1/NA1981.DAT:*
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- 4: /SIDSI/gcgdata/geneseq/emb1/NA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/emb1/NA1984.DAT:*
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- 19: /SIDSI/gcgdata/geneseq/emb1/NA1998.DAT:*
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- 21: /SIDSI/gcgdata/geneseq/emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneseq/emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3826	100.0	3826	24	ABK12806 Human CDNA encodin
2	3420.2	89.4	3436	22	AAH14509 Human CDNA sequenc
3	2322.2	60.7	22893	24	ABK12810 Human tumour suppl
4	2319.8	60.6	5858	22	AAK80624 Human immune/haema
5	2308.6	60.3	30676	24	ABK12811 Human tumour suppl
6	2306.2	60.3	5866	22	AAK80625 Human immune/haema
7	2252.8	58.9	30625	24	ABK12808 Human tumour suppl
8	2252	58.9	5858	22	AAK80626 Human immune/haema

9	995.8	26.0	45845	24	ABK12809	Human tumour suppl
10	838.6	21.9	49744	24	ABK12807	Human tumour suppl
11	592.2	15.5	628	22	AAH06784	Human CDNA clone (
12	562	14.7	573	22	ABA60671	Human foetal liver
13	562	14.7	573	22	ABA28755	Probe #7231 for ge
14	562	14.7	573	22	AAK08953	Human brain expres
15	562	14.7	573	22	AAK34844	Human bone marrow
16	562	14.7	573	22	AAI16850	Probe #6783 for ge
17	562	14.7	573	22	AAI40560	Probe #9246 used t
18	562	14.7	573	22	AB534609	Human liver single
19	562	14.7	573	24	AB509384	Human genome-deriv
20	520.4	13.6	357	22	AAH11818	Human CDNA clone (
21	431	11.3	431	22	ABA73209	Human foetal liver
22	431	11.3	431	22	ABA38642	Probe #17108 for g
23	431	11.3	431	22	AAK1644	Human brain expres
24	431	11.3	431	22	AAK47809	Human bone marrow
25	431	11.3	431	22	AAI76045	Probe #15978 for g
26	431	11.3	431	22	AAI53637	Probe #22323 used
27	431	11.3	431	23	AB547535	Human liver single
28	431	11.3	431	23	AB521816	Human genome-deriv
29	376	9.8	2213	24	AA590400	DNA encoding novel
30	359.4	9.4	371	22	AAK61638	Human immune/haema
31	139.2	3.6	2597	24	AB578645	Human CDNA encodin
32	136.4	3.6	1394	22	AA527383	CDNA encoding nove
33	133	3.5	4181	22	AAAD06778	Human haematopoiet
34	133	3.5	4801	22	AAAD06781	Human haematopoiet
35	132.4	3.5	3038	25	ABX71050	Novel human CDNA s
36	122	3.2	1739	22	AAH64949	Human secreted pro
37	122	3.2	12733	24	ABK8631	Vector pEPF14 con
38	122	3.2	12733	24	ABK8592	Vector pEPF14 cont
39	119.2	3.1	3479	22	AA521305	Human CDNA sequenc
40	119.2	3.1	3479	25	ACA03664	CDNA encoding huma
41	119.2	3.1	3479	25	ACA04085	Human CDNA encodin
42	119.2	3.1	3479	25	ABX89202	DNA encoding novel
43	111.4	2.9	4509	22	AAI07058	Human reproductive
44	111.4	2.9	4509	22	AAK64148	Human immune/haema
45	109.6	2.9	1001	22	AAK61917	Human immune/haema

ALIGNMENTS

RESULT 1	ABK12806	standard; CDNA; 3826 BP.
ID	ABK12806	
XX	ABK12806;	
AC	18-JUN-2002	(first entry)
XX		
DE	Human CDNA encoding tumour suppressor CAR-1.	
XX		
DT		
XX		
KW	Human: ss; tumour suppressor; gene; CAR-1; cytosolic; cancer; tumour;	
KW	gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;	
KW	colon cancer; stomach cancer; breast cancer; endometrial cancer;	
KW	prostate cancer; testicular cancer; ovarian cancer; skin cancer;	
KW	head and neck cancer; oesophageal cancer; bone marrow cancer;	
KW	chromosome 1p31-1p36.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	604..2031
FT		/*tag- a
FT		/product- "CAR-1"
XX		
XX	W0200212285-A2.	
XX		
PN	14-FEB-2002.	
XX		
PD	09-AUG-2001; 2001WO-US25269.	
XX		
PF	10-AUG-2000; 2000US-225033P.	
XX		

PR 23-AUG-2000; 2000US-227560P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Killary A, Chandler D, Loft S;
XX
XX WPI; 2002-269088/31.
DR P-PSDB; AAU78657.
XX
XX New tumour suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumour cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer
PT -
XX
XX Claim 2; Page 134-135; 185pp; English.

The invention relates to an isolated polynucleotide encoding a polypeptide being tumour suppressor, CAR-1. Also included are fragments of the polynucleotide from 15-5000 nucleotides, fragments of the protein from 10-50 amino acids, an expression cassette comprising the polynucleotide under the control of a promoter operable in eukaryotic cells, a method for suppressing growth of a cancer cells by contacting the cells with the expression cassette (i.e. gene therapy), a cell comprising the expression cassette, an anti-CAR-1 monoclonal or polyclonal antibody, a hybridoma cell that produces the monoclonal antibody, a method of diagnosing a cancer by assessing the expression of CAR-1 tumour suppressor in the cells of a tissue sample from a subject, methods for altering the phenotype of a tumour cell, methods for treating a subject with cancer by administering the tumour suppressor CAR-1, or administering a nucleic acid encoding the tumour suppressor CAR-1 and a promoter active in eukaryotic cells, where the promoter is operably linked to the region encoding the tumour suppressor, a non-human transgenic eukaryote lacking a functional CAR-1 gene, a non-human transgenic eukaryote that over-expresses CAR-1 as compared to a similar non-transgenic eukaryote, a method of screening a candidate substance for anti-tumour activity by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance and determining the effect of the candidate substance on the cell, an anti-tumour composition produced by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance, determining the effect of the candidate substance on the cell, identifying a candidate inhibitor substance, and making a composition and/or an isolated and purified nucleic acid that hybridizes, under high stringency conditions, to a DNA segment comprising about 15-3826 bases of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for altering the phenotype of a tumour cell, for treating cancers (e.g. cancer of the brain, lung, liver, kidney, lymph node, pancreas, small intestine, blood cells, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or other tissues), and as a diagnostic or prognostic indicator of cancer. CAR-1 may also be used in screening compounds for activity in either stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the effect of mutant CAR-1 molecule. The gene for CAR-1 is located on chromosome 1 (1p31-1p36). The protein sequence is the cDNA encoding CAR-1.

50 Sequence 3826 BP; 797 A; 1286 C; 999 G; 744 T; 0 other;

Query Match 100.0%; Score 3826; DB 24; Length 3826;

Matches 3826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGGTCGCCCTGAGACCGAGACCGCTGCTGCTAGACATCGCGGGGTAAAGGGTCCCGCTGGG	60
Db	1	AGGTCGCCCTGAGACCGAGACCGCTGCTGCTAGACATCGCGGGGTAAAGGGTCCCGCTGGG	60
QY	61	CCAGGCGTTTGGGGCCCGGGATCCGGCAGCTGAGACGGGCGCGGACCCCTCTCTTCTGTGCC	120
Db	61	CCAGGCGTTTGGGGCCCGGGATCCGGCAGCTGAGACGGGCGCGGACCCCTCTCTTCTGTGCC	120
QY	121	GGTCACAGCCCATGTACGGCTTCGGGCTGAGCTGCCGCCCCACAGGATTTCCCATCCCA	180
Db	121	GGTCACAGCCCATGTACGGCTTCGGGCTGAGCTGCCGCCCCACAGGATTTCCCATCCCA	180

QY	181	GCCTTCGGGCGCCGCCCCGACCGCCCCACCCCGGGATTTCGACACCCCTTAAGGGCTGCAC	240
Db	181	GTTCCTCGCCCTCCCCGACCGCCCCACCCCGGGATTTCGACACCCCTTAAGGGGTCCAC	240
QY	241	CCCGCTCCGGGATCCCTTCTCCAGCTCATCCCTTAAGACTGCCCCGCCCTAGAA	300
Db	241	CCGGGTCCGGGATCCCTTCTCCAGCTCATCCCTTAAGACTGCCCCGCCCTTAGAA	300
QY	301	CTTCCCGGTCAAGGATCTCCGTCCCTCAAGCCGCTCAAGCTCTCTCCAGCCCATTCGCC	360
Db	301	CTTCCCGGTCAAGGATCTCCGTCCCTCAAGCCGCTCAAGCTCTCTCCAGCCCATTCGCC	360
QY	361	TTGAGCTGCCCACTACCTCTAGACTGCCCCCTCCGGGCTGGGGTCCACAGAGTCTCAACC	420
Db	361	TTGAGCTGCCCACTACCTCTAGACTGCCCCCTCCGGGCTGGGGTCCCAAGAGTCTCAACC	420
QY	421	GCGCACCCCTTCTCCGCTTACCCCTCTCCGGAGAGAACCCGCCCTTCTCCGGTATGC	480
Db	421	GCGCACCCCTTCTCCGCTTACCCCTCTCCGGAGAGAACCCGCCCTTCTCCGGTATGC	480
QY	481	TCCTAACCCCTGCTGTGGGGGCTTCGCCGCGCCAGCCCTGGTCTGCTCCAGCA	540
Db	481	TCCTAACCCCTGCTGTGGGGGCTTCGCCGCGCCAGCCCTGGTCTGCTCCAGCA	540
QY	541	GGCGGGGCTCTCTACAGCCGCCCTCTCCCTGGGGCCCCCTCTGTGCTGCCCTGGC	600
Db	541	GGCGGGGCTCTCTACAGCCGCCCTCTCCCTGGGGCCCCCTCTGTGCTGCCCTGGC	600
QY	601	GCCATGGGCTGACAGCTCAAGAGAGGTGCTGCTCATCTGCTCAGATCTACAG	660
Db	601	GCCATGGGCTGACAGCTCAAGAGAGGTGCTGCTCATCTGCTCAGATCTACAG	660
QY	661	GACCCGGTGAAGCTTGGGCTGGAGCACTACTTGCAGCCGCTGCATACAGAGCACTGG	720
Db	661	GACCCGGTGAAGCTTGGGCTGGAGCACTACTTGCAGCCGCTGCATACAGAGCACTGG	720
QY	721	GTGGGGCAGAGGCGGAGGCGCCCGGAGCTGCCCGAGTCCCGGCGCAGCTTGCAGAG	780
Db	721	GTGGGGCAGAGGCGGAGGCGCCCGGAGCTGCCCGAGTCCCGGCGCAGCTTGCAGAG	780
QY	781	CCCGGCTGGGGGCCAGGCTCAAGGTGGCCAACTGAGGCGGTACAGTCTCTCCG	840
Db	781	CCCGGCTGGGGGCCAGGCTCAAGGTGGCCAACTGAGGCGGTACAGTCTCTCCG	840
QY	841	CTGAGCGCATCTTCMAAGCGCGCGCGCGCGGAGCCCTGCAGGCGCAGACAAAGTTC	900
Db	841	CTGAGCGCATCTTCMAAGCGCGCGCGCGCGGAGCCCTGCAGGCGCAGACAAAGTTC	900
QY	901	AAAGCTCTTCTGCTCAGGAGCCGGCGCTTCTTGTCTTCTTCTGCGAGAGCTTGCAGTG	960
Db	901	AAAGCTCTTCTGCTCAGGAGCCGGCGCTTCTTGTCTTCTTCTGCGAGAGCTTGCAGTG	960
QY	961	CACGAGCAGATCAAGGTGACCGGGATGAGAGAGCGCTTCGACGAGTGCACAAAGGAGTGTG	1020
Db	961	CACGAGCAGATCAAGGTGACCGGGATGAGAGAGCGCTTCGACGAGTGCACAAAGGAGTGTG	1020
QY	1021	AAGGACCAACTTCAGGCGCTTCAAGAGACAGCAGGCGGAAACACACCGAGGCGCTCAGCTG	1080
Db	1021	AAGGACCAACTTCAGGCGCTTCAAGAGACAGCAGGCGGAAACACACCGAGGCGCTCAGCTG	1080
QY	1081	CTCAAGCAGACAATGGCGGAGACCAAGTCTTTCACACAAAGAGCTGCGGAGCACTATGGC	1140
Db	1081	CTCAAGCAGACAATGGCGGAGACCAAGTCTTTCACACAAAGAGCTGCGGAGCACTATGGC	1140
QY	1141	GAGGCTTTCAGGCGGCTGACACGGCTGTGTGTAAAGCCAGAAAGGCGCTCTAGAGAG	1200
Db	1141	GAGGCTTTCAGGCGGCTGACACGGCTGTGTGTAAAGCCAGAAAGGCGCTCTAGAGAG	1200
QY	1201	CTGAGAGGCGAGCGGCGCGCAGCTGACAGCATCTGAGAGAAAGTCCAGCGCTTACAGC	1260
Db	1201	CTGAGAGGCGAGCGGCGCGCAGCTGACAGCATCTGAGAGAAAGTCCAGCGCTTACAGC	1260
QY	1261	CAGAGCTGCGCAAGGTTCAGAGAGGAGCCAGATCTCTGACAGAGCGGCTTGGAAACC	1320


```

1261 CAGCAGCTGCGAAGGTCAGAGGAGGAGCCAGATCTCAGAGAGGGGTGGCTGAAACC 1320
1321 GACCGGACACACCTTCCTGGGCTGGGGTGCCCTCACTGTCCGAGCGGCTCAAGGAAAAATC 1380
1322 GACCGGACACACCTTCCTGGGCTGGGGTGCCCTCACTGTCCGAGCGGCTCAAGGAAAAATC 1380
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1381 CATGAGACCAACCTCAATATGAAAGATCTCCGACCTCCAGTATACAGAGCCCTCCGACG 1440
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1501 GACCCGGGACACGCCACAGCGGCTGATCTGTGCGAGAGTGCACCAATGTGGCTTAC 1560
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1561 GGCACACTTGACCCACAGCAGCTGACAGACTCGCCAAAGCGCTTCAGTGTGAGGTGTG 1620
1561 GGCACACTTGACCCACAGCAGCTGACAGACTCGCCAAAGCGCTTCAGTGTGAGGTGTG 1620
1621 GTGCTGGGTCTGAAGCCTTCACTAGTGGCTCCACTACTGGAGGTGGTGGGCGAG 1680
1621 GTGCTGGGTCTGAAGCCTTCACTAGTGGCTCCACTACTGGAGGTGGTGGGCGAG 1680
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1861 CTGGAATATGACCAAGGCTTGTCTATCTTCTACAAATGTGTATGATGATGCTGGCTTAC 1920
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1921 ACCTTCCGAGAAAGTTCCTTGGCAAGCTCTGCTTACTTACAGCCCTGGCCAGAGCCAC 1980
1921 ACCTTCCGAGAAAGTTCCTTGGCAAGCTCTGCTTACTTACAGCCCTGGCCAGAGCCAC 1980
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1981 GCCAATGGCAAGAGTTCAGCGGCTGGGAGTCAACAGCTCCGCACTGATGTCAGAGCAG 2040
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2041 AAGGAGACCAACCTTCCTGGAGCACTGCACTGCAAGAGCCCTGGCCAGAGAAATAG 2100
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2101 AAGAGCTGAGACTCAGAGCCAGCTGGCACTGCAAGAGCTCAGAGCCAGTTGTTTACCTCC 2160
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2161 AGCCTCAGAGTCTGTAATATGAGAGTTCCTTCACTTCTAACTCTCTCCAGCATC 2220
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2221 GATGTTCTGATAGCTGACCTTGTATAGGATACAGTTTGTATCAAGAGATGATGATG 2280
2281 GATGTTCTGATAGCTGACCTTGTATAGGATACAGTTTGTATCAAGAGATGATGATG 2340
2281 GATGTTCTGATAGCTGACCTTGTATAGGATACAGTTTGTATCAAGAGATGATGATG 2340
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2401 AGTTGGACAGCCCGAAGACACACAGCAGCCCTTATATGTCATGAGGCTTAAGATTCGCC 2460
2461 TGAACAGCTAGTATGAGGCACTTATACCTTGAACCCAGTCCACAGTGTATCAGAGTAGT 2520
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2581 ATGTTCTCTACTTCTCCCACTGATCTGCTGAGTCAAGATGATGATGCTGGCTGGAGAG 2640
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2641 CACCTGTAGTGAAGTTCACACATATATAGTATGATGATGATGATGATGATGATGATG 2700
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2761 GAGGAGCAGGCTGAGGCTATACCCAAAGCTGATGATGATGATGATGATGATGATGATG 2820
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3001 GACAGAGATTTACTACCTGGCCCTGGTGGCTTGCAGAAATGTTTGAAGAGCTGAGAG 3060
3001 GACAGAGATTTACTACCTGGCCCTGGTGGCTTGCAGAAATGTTTGAAGAGCTGAGAG 3060
3061 GACAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
3061 GACAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
3121 GGAAGAGTCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
3121 GGAAGAGTCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
3181 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
3181 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
3241 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
3241 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
3301 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
3301 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
3361 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
3361 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
3421 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
3421 GGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
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OY 3481 AGTGGGAACGTGAGAGAGTGGGCTGCAAGACTGAGCCCTAAATGCTCTCCCGGCTTGACT 3540
 DB 3481 AGTGGGAACGTGAGAGAGTGGGCTGCAAGACTGAGCCCTAAATGCTCTCCCGGCTTGACT 3540
 OY 3541 TTTCTTTCTACTGCTGGGGCTTACATTTCTGACCTTGGGGCTCTGACACACACACACTC 3600
 DB 3541 TTTCTTTCTACTGCTGGGGCTTACATTTCTGACCTTGGGGCTCTGACACACACACACTC 3600
 OY 3601 CCAAGTAGAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGAGTGGCCCGCCACCCG 3660
 DB 3601 CCAAGTAGAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGAGTGGCCCGCCACCCG 3660
 OY 3661 GGCTCTCCCTGGGCAAAAGAAATGTCAGCCCTACCCACCCCTCAACTACAGAAATCT 3720
 DB 3661 GGCTCTCCCTGGGCAAAAGAAATGTCAGCCCTACCCACCCCTCAACTACAGAAATCT 3720
 OY 3721 GGGCCACCCCGAGAGTATTTTAAATGTTGGCCATTTAAATGACTTAAATGATCAAT 3780
 DB 3721 GGGCCACCCCGAGAGTATTTTAAATGTTGGCCATTTAAATGACTTAAATGATCAAT 3780
 OY 3781 TGTATTAATTAAGTTACAGATGTCAAAAAAATTTTAAAAA 3826
 DB 3781 TGTATTAATTAAGTTACAGATGTCAAAAAAATTTTAAAAA 3826

RESULT 2
 AAH14509 standard; cDNA: 3436 BP.

AAH14509:
 26-JUN-2001 (first entry)
 Human cDNA sequence SEQ ID NO:12036.
 Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens.
 EP1074617-A2.
 07-FEB-2001.
 28-JUL-2000; 2000EP-0116126.
 29-JUL-1999; 99JP-0248036.
 27-AUG-1999; 99JP-0300253.
 11-JAN-2000; 2000JP-018776.
 09-JUN-2000; 2000JP-0183767.
 09-JUN-2000; 2000JP-0241899.
 (HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;
 WPI: 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602
 full-length cDNAs defined in the specification, and for the detection
 and/or diagnosis of the abnormality of the proteins encoded by the
 full-length cDNAs -
 Claim 8; SEQ ID 12036; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesizing 5602
 full-length cDNAs defined in the specification. Where a primer set
 comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 to the complementary strand of a polynucleotide which comprises one of
 the 5602 nucleotide sequences defined in the specification, where the
 oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end
 sequence and an oligonucleotide comprising a sequence complementary to a
 polynucleotide which comprises a 3'-end sequence, where the
 oligonucleotide comprises at least 15 nucleotides and the combination of
 the 5'-end sequence/3'-end sequence is selected from those defined in
 the specification. The primer sets can be used in antisense therapy and
 in gene therapy. The primers are useful for synthesizing polynucleotides,
 particularly full-length cDNAs. The primers are also useful for the
 detection and/or diagnosis of the abnormality of the proteins encoded by
 the full-length cDNAs. The primers allow obtaining of the full-length
 cDNAs easily without any specialised methods. AAH13632 to AAH13632
 AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632
 represent oligonucleotides, all of which are used in the exemplification
 of the present invention.

Sequence 3436 BP: 731 A; 1126 C; 901 G; 678 T; 0 other;

Query Match 89.4%; Score 3420.2; DB 22; Length 3436;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 370 CCAGTACCTTAGAGTGGCCCTCCGGGCTGGGCTCCAGAGATCTACCGCCGACCC 429
 DB 1 CCAGTACCTTAGAGTGGCCCTCCGGGCTGGGCTCCAGAGATCTACCGCCGACCC 60
 OY 430 TTCCCTCGGCTTACCTCTCTCCGAGACACACCCCTCTCTCCGCTAGCTCTACCC 489
 DB 61 TTCCCTCGGCTTACCTCTCTCCGAGACACACCCCTCTCTCCGCTAGCTCTACCC 120
 OY 490 TGCCTGTGGGCTCGTCCCGGCGCCAGCCCTGCGTGTGCTCCGACAGCCCGCC 549
 DB 121 TGCCTGTGGGCTCGTCCCGGCGCCAGCCCTGCGTGTGCTCCGACAGCCCGCC 180
 OY 550 TCTCTCAGCGCCGCCCTCCGCTGGGCGCCCTCTGCTGTGCGCCGCGCATGGCG 609
 DB 181 TCTCTCAGCGCCGCCCTCCGCTGGGCGCCCTCTGCTGTGCGCCGCGCATGGCG 240
 OY 610 TGCAGCTCAAGAGAGAGCTGTGCTCATCTGCTGAGACATCTACAGAGACCGGTG 669
 DB 241 TGCAGCTCAAGAGAGAGCTGTGCTCATCTGCTGAGACATCTACAGAGACCGGTG 300
 OY 670 AGCTGTGGCTCGAGACACTTCTTGGCGCCGCTGCTACAGAGACACTGGGTGCGGAG 729
 DB 301 AGCTGTGGCTCGAGACACTTCTTGGCGCCGCTGCTACAGAGACACTGGGTGCGGAG 360
 OY 730 GAGCGGAGGCGCCGCGGCTGCGGAGTGGCGGCGGAGGCTTGGCGGAGCCGCGGTG 789
 DB 361 GAGCGGAGGCGCCGCGGCTGCGGAGTGGCGGCGGAGGCTTGGCGGAGCCGCGGTG 420
 OY 790 GCGCCAGCCTCAAGCTGCGGACATGCTGAGAGGCTACAGCTCTCCGCTGAGAGCC 849
 DB 421 GCGCCAGCCTCAAGCTGCGGACATGCTGAGAGGCTACAGCTCTCCGCTGAGAGCC 480
 OY 850 ATCTCTCAAGCGGCGCGCGGCGGCGGAGCTTGGCGGCGGAGGCTTGGCGGAG 909
 DB 481 ATCTCTCAAGCGGCGCGCGGCGGCGGAGCTTGGCGGCGGAGGCTTGGCGGAG 540
 OY 910 TGCCTCAGGAGCGCGGCGCTTCTGCTTCTTGGCGGAGGCTTGGCGGAGGAG 969
 DB 541 TGCCTCAGGAGCGCGGCGCTTCTGCTTCTTGGCGGAGGCTTGGCGGAGGAG 600
 OY 970 CATCAGGTCAACCGGATCAGAGAGCTTGGAGAGTGAAGAGGAGGAGGAGGAGCA 1029
 DB 601 CATCAGGTCAACCGGATCAGAGAGCTTGGAGAGTGAAGAGGAGGAGGAGGAGCA 660
 OY 1030 CTTGAGGCGCTTCAAGACAGGAGCGGAGACACACCGAGGCTGAGCTCTCAACGA 1089
 DB 661 CTTGAGGCGCTTCAAGACAGGAGCGGAGACACACCGAGGCTGAGCTCTCAACGA 720
 OY 1090 CAATGTGGGAGAGCAAGTCTTCCACCAAGAGCTTGGAGGAGGAGGAGGAGGCTT 1149
 DB 721 CAATGTGGGAGAGCAAGTCTTCCACCAAGAGCTTGGAGGAGGAGGAGGAGGAGGCTT 780

QY 1150 GAGCGGCTGCACCGGCTGCTGCGGTGAACCCAGAAAGCCATGCTAGAGAGCTGAGAGCG 1209
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QY 1210 GACAGCGGCGGACCGGTGACCGGACATCGAGGAAAGTCCAGCGGTCACGCGCAGCGAGCTG 1269
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Db 841 GACAGCGGCGGACCGGTGACCGGACATCGAGGAAAGTCCAGCGGTCACGCGCAGCGAGCTG 900
| | | | |
QY 1270 GCGAAGGTCCAGAGGAGGAGCCAGATCTGTCAGAGAGCGGCTGGCTGAAACCCAGCGGAC 1329
| | | | |
Db 901 GCGAAGGTCCAGAGGAGGAGCCAGATCTGTCAGAGAGCGGCTGGCTGAAACCCAGCGGAC 960
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| | | | |
Db 961 ACCCTTCCTGGCTGGGGTGGCTCTACTGTCCGAGCGGCTCAAGGGAAAAATCCATGAGACC 1020
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Db 1081 TGGAAAGTCCCTGTTCAGAGACATCCACCGAGTCCAGCGGCTTAACCTGAGACCGGCG 1140
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| | | | |
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| | | | |
QY 1870 GACCAAGGCTTGCTCACTCTTCAATGCTGATGACATGTCTGCTTACACCTTCCGC 1929
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QY 2170 TCTGTAAATGAGAGTGTGATCTCTAACTCTCTCAGAGCATGAGTGTCTG 2229
| | | | |
Db 1800 TCTGTAAATGAGAGTGTGATCTCTAACTCTCTCAGAGCATGAGTGTCTG 1859
| | | | |

QY 2230 TAGCTTGACCTTGATAGGATACAGCTTTGATCCAGAGATGTGACATGGCTTCTCTCA 2289
| | | | |
Db 1860 TAGCTTGACCTTGATAGGATACAGCTTTGATCCAGAGATGTGACATGGCTTCTCTCA 1919
| | | | |
QY 2290 GGGCAACCCCTGGCCAAACCTCAATCCATCTTCAAGGGGAGGGGAGCTACCTTCAGT 2349
| | | | |
Db 1920 GGGCAACCCCTGGCCAAACCTCAATCCATCTTCAAGGGGAGGGGAGCTACCTTCAGT 1979
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QY 2350 GTCTCCCTCAGCCAGCCCTGACCTCAGAAAGTGCAGAGCATGTGCGCATAGTTGGAG 2409
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QY 2410 CCGGAAAGACACACAGACCTCTTATGTGCCATGAGCCTTAAGACTTAACCTGACCAAGC 2469
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QY 3250 GTTCCCAATCTAAATTTTACAGAGATCTGTTGGGGAATTAAGTCAGATCCAGA 3309
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Db 2880 GTTCCCAATCTAAATTTTACAGAGATCTGTTGGGGAATTAAGTCAGATCCAGA 2939
| | | | |
QY 3310 ACCTTGGCTGCAAGGAGTCTGGGAAATGTCAATTCCTAGAAAGAAATTAGGCTGGCTG 3369
| | | | |

D	b		2940	ACCTTGGGTGCAGGAGACTCGGGAAATGTCATCCTCCATAAGAATTAGGGTG	2999
Oy			3370	GAGCAAGCCCCAACCCTGCCGTTTTTTCTGCCACAACATCCAATGTAAGAACTGGGAGAGG	3429
D	b		3000	GAGCAAGCCCCAACCTCGCTTTTTTCTGCCACAGCATCCAAATGTGAAGAACTGGGAGAGG	3059
Oy			3430	GTGAGTAGCACATCTAGGGTTGGCTGCCCTTGCCCTGTATCCCCTGCACAGAGTGGGAA	3489
D	b		3060	GTGAGTAGCACATCTAGGGTTGGCTGCCCTTGCCCTGTATCCCCTGCACAGAGTGGGAA	3119
Oy			3480	CTGAGAGAGTGGGCTGCCAAGACTGAGCTAAATGTCTCCCGGCTTGACTTTCTTTCT	3549
D	b		3120	CTGAGAGAGTGGGCTGCCAAGACTGAGCTAAATGTCTCCCGGCTTGACTTTCTTTCT	3179
Oy			3550	AGTCTGGGGCTGATCTGCACTGGGGGTCTGACACAAACACACATCCCAAATGAG	3609
D	b		3180	AGTCTGGGGCTGATCTGCACTGGGGGTCTGACACAAACACACATCCCAAATGAG	3239
Oy			3610	CCGGAAGAGCTAAACACAGGGGGTCTTTAAAATGGTGCSCCCGCCAACCCGGGCTCCT	3669
D	b		3240	CCGGAAGAGCTAAACACAGGGGGTCTTTAAAATGGTGCSCCCGCCAACCCGGGCTCCT	3299
Oy			3670	TGGGCAAAAGAAATGTTGACGCCCTTAACCCCAACCCTTCACTACAGAAATCGGCCACCC	3729
D	b		3300	TGGGCAAAAGAAATGTTGACGCCCTTAACCCCAACCCTTCACTACAGAAATCGGCCACCC	3359
Oy			3730	CAGCAGATTTTATTTTAAAAATGTTGCCATTTATGATGATGATCAATTTGATTTAA	3789
D	b		3360	CAGCAGATTTTATTTTAAAAATGTTGCCATTTATGATGATGATCAATTTGATTTAA	3419
Oy			3790	TTAAAGTTACAGATGTC 3806 	
D	b		3420	TTAAAGTTACAGATGTC 3436	
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R	E	S	I	L	A
RESULT 3					
FH	ID	ABK12810	standard; DNA:	22893 BP.	
P	X	ABK12810;			
D	E	18-JUN-2002	(first entry)		
KW	DE	Human tumour suppressor CAR-1,	BAC clone RP11-150F21 3'	sequence.	
KM	XX	Human; ds; tumour suppressor; CAR-1;	cytostatic; cancer; tumour;		
KV	KW	gene therapy; brain cancer; lung cancer;	liver cancer; kidney cancer;		
KX	KW	colon cancer; stomach cancer; breast cancer;	endometrial cancer;		
KY	KW	prostate cancer; testicular cancer; ovarian cancer;	skin cancer;		
KZ	KW	head and neck cancer; esophageal cancer;	dome marrow cancer; BAC;		
LA	KW	bacteria artificial chromosome; chromosome lp31-lp36.			
LB	OS	Homo sapiens.			
LC	XX				
LD	FH	Key	Location/Qualifiers		
LE	FT	misc_feature	5820		
LF	FT	/tag= "note= "	Nucleotides 5821-6360 of the present		
LG	FT	sequence as reproduced in the specification are illegible			
LH	FT	or missing; nucleotide 5821 of the present sequence			
LJ	FT	corresponds to nucleotide 6361 of sequence as printed in			
LK	FT	the specification"			
LL	PN	WO200212285-A2.			
LM	XX				
LN	PD	14-FEB-2002.			
LO	PF	09-AUG-2001; 2001MO-US25269.			
LP	PR	10-AUG-2000; 2000US-225033P.			
LQ	PR	23-Aug-2000; 2000US-227560P.			
LR	XX				

(TEKA) UNIV TEXAS SYSTEM.

Killary A, Chandler D, Iott S;
WPI; 2002-26908/31.

New tumour suppressor CAR-1 polypeptides and polynucleotides, useful for diagnosing cancer, for altering the phenotype of a tumour cell, for treating cancers or as a diagnostic or prognostic indicator of cancer

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Disclosure; Page 170-176; 185pp; English.

The invention relates to an isolated polynucleotide encoding a polypeptide being tumour suppressor, CAR-1. Also included are fragments of the polynucleotide from 15-500 nucleotides, fragments of the protein from 10-50 amino acids, an expression cassette comprising the polynucleotide under the control of a promoter operable in eukaryotic cells, a method for suppressing growth of a cancer cells by contacting the cells with the expression cassette (i.e. gene therapy), a cell comprising the expression cassette, an anti-CAR-1 monoclonal or polyclonal antibody, a hybridoma cell that produces the monoclonal antibody, a method of diagnosing a cancer by assessing the expression of CAR-1 tumour suppressor in the cells of a tissue sample from a subject, methods for altering the phenotype of a tumour cell, methods for treating a subject with cancer by administering the tumour suppressor CAR-1, or by administering a nucleic acid encoding the tumour suppressor CAR-1 and a promoter active in eukaryotic cells, where the promoter is operably linked to the region encoding the tumour suppressor, a non-human transgenic eukaryote lacking a functional CAR-1 gene, a non-human transgenic eukaryote that over-expresses CAR-1 as compared to a similar non-transgenic eukaryote, a method of screening a candidate substance for anti-tumour activity by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance and determining the effect of the candidate substance on the cell, an anti-tumour composition produced by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance, determining the effect of the candidate substance on the cell, identifying a candidate inhibitor substance, and making a composition and an isolated and purified nucleic acid that hybridizes, under high stringency conditions, to a DNA segment comprising about 15-3826 bases of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for altering the phenotype of a tumour cell, for treating cancers (e.g. cancer of the brain, lung, liver, kidney, lymph node, pancreas, small intestine, blood cells, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or other tissues), and as a diagnostic or prognostic indicator of cancer. CAR-1 may also be used in screening compounds for activity in either stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the effect of mutant CAR-1 molecule. The gene for CAR-1 is located on chromosome 1 (1p1-1p36). The present sequence is a BAC (bacterial artificial chromosome) containing part of the CAR-1 gene.

SQ Sequence .22893 BP; 5720 A; 5989 C; 5664 G; 5415 T; 105 other;

Query Match Best Local Similarity 60.7%; Score 2322.2; DB 24; Length 22893; Matches 2350; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

1429 GCCCCCTGCGAGTGCACCATCTGGAAATCCTTCCTTGCCAGACATCCACCAGTGCAGCC 1488
||||| | | | | | | | | | | | | | | | | | | | | |
Db 11940 GTGCCACAGCCTTCCTGCCCACTCATCTCTCTCTCTCTCCACACCCCACAGTGCAGCC 11999

1489 GCCCTAACCTGGAACCCGGGACAGCCCCACAGCGCTGATCTCTGTGGACGACTGCACC 1548

Db 12000 GCCCTAACCTGTGAGCCGGGACAGCCCCACAGCGCTGATCTCTGTGGACGACTGCACC 12055

1549 ATTGTGGCTTAAGCGCACTTGACACCCAGCACACTGAGGACATCGCCAAGCGCTTCGAT 1608
||||| | | | | | | | | | | | | | | | | | | | | |
Db 12060 ATTGTGGCTTAAGCGCACTTGACACCCAGCACACTGAGGACATCGCCAAGCGCTTCGAT 12119

1609 GTGAGAGTGTCTCGAGTCTGGAGTCTTGAAGCCCTTAGTAGTGGCTCTCACTACTGGAGAGTG 1668
||||| | | | | | | | | | | | | | | | | | | | | |
DB 12120 GTGAGAGTGTCTCGAGTCTGGAGTCTTGAAGCCCTTAGTAGTGGCTCTCACTACTGGAGAGTG 12177

OY	1669	GTGGTGGCGGAGAAAGACCAGTGGGTGATCGGGCTGGCACAGAGAAACCCCAAGCCGCAAG	1728
Db	12180	GTGGTGGCGGAGAAAGACCAGTGGGTGATCGGGCTGGCACAGAGAAACCCCAAGCCGCAAG	12239
OY	1729	GGCAGCATCCAGATCCAGCCCAAGCCGGGCTTCTACTGCATCGTGATGCAGATGGCAAC	1788
Db	12240	GGCAGCATCCAGATCCAGCCCAAGCCGGGCTTCTACTGCATCGTGATGCAGATGGCAAC	12299
OY	1789	CAGTACAGCGCCCTGCACAGGAGCCCTGGACCGGGCTTAAGTCCTGGGACAAGCTTGACAG	1848
Db	12300	CAGTACAGCGCCCTGCACAGGAGCCCTGGACCGGGCTTAAGTCCTGGGACAAGCTTGACAG	12359
OY	1849	GTGGGTCTCTTCCCTGGAGCTATGACCAAGGCTTCTCATCTCTACAACTCGTATGACATG	1908
Db	12360	GTGGGTCTCTTCCCTGGAGCTATGACCAAGGCTTCTCATCTCTACAACTCGTATGACATG	12419
OY	1909	TCTGTGCTCTACACCTTCCGCGAAGATTCCCTGGCAAGCTCTGCTCTTACTTCAAGCCCT	1968
Db	12420	TCTGTGCTCTACACCTTCCGCGAAGATTCCCTGGCAAGCTCTGCTCTTACTTCAAGCCCT	12479
OY	1969	GGCCAGAGCCACCGCCAAATGGCAAGAAGCTTCAAGCCCTGGGATCAACACGTCGGCATC	2028
Db	12480	GGCCAGAGCCACCGCCAAATGGCAAGAAGCTTCAAGCCCTGGGATCAACACGTCGGCATC	12539
OY	2029	TAGTCCAGGGCAGAGGAGACACAAACCTCTGGGACACATGGCAACCTGGCAAGGCCCTGC	2088
Db	12540	TAGTCCAGGGCAGAGGAGACACAAACCTCTGGGACACATGGCAACCTGGCAAGGCCCTGC	12599
OY	2089	CCAGGAAGATAGAAAGACTGGACTGCACGCCACGTCGACACTGGAGACTGAGACTGAGCCAGT	2148
Db	12600	CCAGG - AGATAGAAAGACTGGACTGCACGCCACGTCGACACTGGAGACTGAGACTGAGCCAGT	12658
OY	2149	TGTTTACCCTTCAGACCTTCACAGTCTGTAAAAATGGAAGTTGCATTCCCTACTTCCTAACTC	2208
Db	12659	TGTTTACCCTTCAGACCTTCACAGTCTGTAAAAATGGAAGTTGCATTCCCTACTTCCTAACTC	12718
OY	2209	TCTTCCAGACATGCATGTCTGTAGCTCTGACCTTGATAGGAGATACAGCTTGTATCCAAAG	2268
Db	12719	TCTTCCAGACATGCATGTCTGTAGCTCTGACCTTGATAGGAGATACAGCTTGTATCCAAAG	12778
OY	2269	ATGTGACATGAGCTTCTCTCAGGGGCAACCCCTGCGCAACCCCTATCCCATCTTCTCAGG	2328
Db	12779	ATGTGACATGAGCTTCTCTCAGGGGCAACCCCTGCGCAACCCCTATCCCATCTTCTCAGG	12838
OY	2329	GGCAGGGGACTACTTCTCAATGTCTCTCCCTCAAGCCCAAGCCCTGACCTCAAGAAATGTCAAG	2388
Db	12839	GGCAGGGGACTACTTCTCAATGTCTCTCCCTCAAGCCCAAGCCCTGACCTCAAGAAATGTCAAG	12898
OY	2389	AGCATGGCCAGTAGTGGGAGCCCGAAAGACACAGCAAGCCCTTAATGCCATAGGCCCT	2448
Db	12889	AGCATGGCCAGTAGTGGGAGCCCGAAAGACACAGCAAGCCCTTAATGCCATAGGCCCT	12958
OY	2449	AAGACTTACCCTTGACCAAGCTAGTGTGGGCCATTACTCTTGAACCCCAAGTCCACAGTG	2508
Db	12959	AAGACTTACCCTTGACCAAGCTAGTGTGGGCCATTACTCTTGAACCCCAAGTCCACAGTG	13018
OY	2509	GTCACAGGTAGTACTCTGTGCTTACGTTGCTCTGAGAGCCAAAGCTCTCTGCCACCCCCAC	2568
Db	13019	GTCACAGGTAGTACTCTGTGCTTACGTTGCTCTGAGAGCCAAAGCTCTCTGCCACCCCCAC	13078
OY	2569	ACCAAGAACTAATATGATGCTTACTTGTCCCAACGATCTGTGGTCAGTATATGCTGTGG	2628
Db	13079	ACCAAGAACTAATATGATGCTTACTTGTCCCAACGATCTGTGGTCAGTATATGCTGTGG	13138
OY	2629	GCCGTGTGAAGGCAACCTGTAGTTGAGTCCACACATTAATAGTCATGTGCACACACTTTC	2688
Db	13139	GCCGTGTGAAGGCAACCTGTAGTTGAGTCCACACATTAATAGTCATGTGCACACACTTTC	13198
OY	2689	TGCCCAACAGGCCGAGGAGCAAGGGTGAAGGGTATACCCAAAGCTGATCAGAGCCCATTAAGC	2748
Db	13199	TGCCCAACAGGCCGAGGAGCAAGGGTGAAGGGTATACCCAAAGCTGATCAGAGCCCATTAAGC	13258

QY	2749	CTAAAGCACTGCAGACAAAGCCTCCCTGGATATGAGAGTCCCCAGTAGCTGTGAACA	2808
Db	13259	CTAAAGCACTGCAGACAAAGCCTCCCTGGATATGAGAGTCCCCAGTAGCTGTGAACA	1331
QY	2809	AGAGCCAGCCAAACCCTCTTCAAGCAGGCGCTGTGACCTGTAGAGGTGCGAGAGGCTTC	2868
QY	2869	CAGAAGCAGTGTGTATTTAGGACCCAGACACTGGGAGGGGCTGTTGGCTAGACCCCTT	2928
Db	13379	CAGAAGCAGTGTGTATTTAGGACCCAGACACTGGGAGGGGCTGTGGCTAGACCCCTT	1343
QY	2929	GTCAAGACTTGGCATCTATCTCAGTTAGATCTCTGTGCAGAAAACAAGACCACTTGTAG	2988
Db	13439	GTCAAGACTTGGCATCTATCTCAGTTAGATCTCTGTGCAGAAAACAAGACCACTTGTAG	1349
QY	2989	CTGGTTTAATTAGACAAGATTTACTACTCTGGCCCTGTGTGGCTTGCAAAATTGTGGAA	3048
Db	13499	CTGGTTTAATTAGACAAGATTTACTACTCTGGCCCTGTGTGGCTTGCAAAATTGTGGAA	1355
QY	3049	GAGCGGAGGAGACAGACTCTGTGAAATTTCCAGAACTCCAGGGCCAGATTCATCATGT	3108
Db	13559	GAGCTGGAGAACAGACTCTGTGAAATTTCCAGAACTCCAGGGCCAGATTCATCATGT	1361
QY	3109	CTGTGTGACCAAGAGAAAGCTGCCCATCTGCAGAAAGCCACTATGCCAGAAACCTACTG	3168
Db	13619	CTGTGTGACCAAGAGAAAGCTGCCCATCTGCAGAAAGCCACTATGCCAGAAACCTACTG	1367
QY	3169	ACTGCAGAACTAGGCTCCCTGTGCCACGGTCCGTGCCAGCCCAATAGATGTCTGAGGCT	3228
Db	13679	ACTGCAGAACTAGGCTCCCTGTGCCACGGTCCGTGCCAGCCCAATAGATGTCTGAGGCT	1373
QY	3229	GCCCTCTCCCACTTCACTCAATGCCAAATCTAAATTTTACAAAGATCTGTGGG	3288
Db	13739	GCCCTCTCCCACTTCACTCAATGCCAAATCTAAATTTTACAAAGATCTGTGGG	1379
QY	3289	GGAACCTTAAGTCAGATCCAGAACTTGGCTCAAGAGAGTGTGGGAAATGTCAATTCCT	3348
Db	13799	GGAACCTTAAGTCAGATCCAGAACTTGGCTCAAGAGAGTGTGGGAAATGTCAATTCCT	1385
QY	3349	AGAAAGAAATTAGGGTGGGTGGAGCAAGCCCACTGCGTTTCTGCCACAGATCCAA	3408
Db	13859	AGAAAGAAATTAGGGTGGGTGGAGCAAGCCCACTGCGTTTCTGCCACAGATCCAA	1391
QY	3409	TCTGTAACAACCTCGGGAAGGGTGGAGTCCACATCTAGGGTGTCTGCGCCCTGGCTCT	3468
Db	13919	TCTGTAACAACCTCGGGAAGGGTGGAGTCCACATCTAGGGTGTCTGCGCCCTGGCTCT	1397
QY	3469	ATCCCTGGCCAGAGGTGGGAAGTGGAGAGTGGCTGGAACAGTGAAGCTTAATGTCTCC	3528
Db	13979	ATCCCTGGCCAGAGGTGGGAAGTGGAGAGTGGCTGGAACAGTGAAGCTTAATGTCTCC	1403
QY	3529	CCGGCTTGACTTTCTTCTAGTCTGTGGGCTAGATTTGCACTTGGGGTCTGTGACA	3588
Db	14039	CCGGCTTGACTTTCTTCTAGTCTGTGGGCTAGATTTGCACTTGGGGTCTGTGACA	1409
QY	3589	CAACACACATCCCAAAAGTACCGGAGAGACTTAAACACAGGGGTTCTTTAAATGTGCTC	3648
Db	14099	CAACACACATCCCAAAAGTACCGGAGAGACTTAAACACAGGGGTTCTTTAAATGTGCTC	1415
QY	3649	CCCGGCCACCGGGGCTCCCTTGGGCAAAAGAAATGTCAACCCCTACCCCAACCCCTCAA	3708
Db	14159	CCCGGCCACCGGGGCTCCCTTGGGCAAAAGAAATGTGTACACCCCTACCCCAACCCCTCAA	1421
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Db	14219	CTACAGAACTGGGCCACCCACAGACTATTTTAAATTTTAAATGTGCCATTTTATGAG	1427
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RESULT 4
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ID AAK80624 standard; DNA; 5858 BP.
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XX 07-NOV-2001 (first entry)
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:35436.
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XX Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
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OS Homo sapiens.
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Oy      2973 CAAGAGCCACTGTGTAGCTGTTTAAATTAACAAGATTTTACTAGCTGGCCCTGTGGCT 3032
Db      1500 CAAAGCCCACTGTGTAGCTGTTTAAATTAACAAGATTTTACTAGCTGGCCCTGTGGCT 1559
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Db      2220 TACCCTAACCTTCAACTACAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2279
Oy      3753 TTGCCCATTTTATGAGTTATGATCAATTTTGTATTAATTAAGTTACAGATGTCA 3807
Db      2280 TTGCCCATTTTATGAGTTATGATCAATTTTGTATTAATTAAGTTACAGATGTCA 2334

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RESULT 5
ABK12811
ID      ABK12811 standard; DNA: 30676 BP.
XX
AC      ABK12811;
XX
DT      18-JUN-2002 (first entry)
XX
DE      Human tumour suppressor CAR-1, BAC clone RP11-131M1.
XX
KW      Human; ds: tumour suppressor; CAR-1; cytosolic; cancer; tumour;
KW      gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW      colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW      prostate cancer; testicular cancer; ovarian cancer; skin cancer;

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KW      head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW      bacteria artificial chromosome; chromosome 1p31-1p36.
XX
OS      Homo sapiens.
XX
PN      MO200212285-A2.
XX
PD      14-FEB-2002.
XX
PF      09-AUG-2001; 2001WO-US25269.
XX
PR      10-AUG-2000; 2000US-225033P.
PR      23-AUG-2000; 2000US-227560P.
XX
PA      (TEXA ) UNIV TEXAS SYSTEM.
PI      Killary A, Chandler D, Lott S;
XX
DR      WPI; 2002-269088/31.
XX
PT      New tumour suppressor CAR-1 polypeptides and polynucleotides, useful for
PT      diagnosing cancer, for altering the phenotype of a tumour cell, for
PT      treating cancers or as a diagnostic or prognostic indicator of cancer
XX
PS      Disclosure; Page 176-185; 185pp; English.
XX
XX
XX      The invention relates to an isolated polynucleotide encoding a
XX      polypeptide being tumour suppressor, CAR-1. Also included are
XX      fragments of the polynucleotide from 15-5000 nucleotides, fragments of
XX      the protein from 10-50 amino acids, an expression cassette comprising the
XX      polynucleotide under the control of a promoter operable in eukaryotic
XX      cells, a method for suppressing growth of a cancer cells by contacting
XX      the cells with the expression cassette (i.e. gene therapy), a cell
XX      comprising the expression cassette, an anti-CAR-1 monoclonal or
XX      polyclonal antibody, a hybridoma cell that produces the monoclonal
XX      antibody, a method of diagnosing a cancer by assessing the expression of
XX      CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
XX      methods for altering the phenotype of a tumour cell, methods for treating
XX      a subject with cancer by administering the tumour suppressor CAR-1, or by
XX      administering a nucleic acid encoding the tumour suppressor CAR-1 and a
XX      promoter active in eukaryotic cells, where the promoter is operably
XX      linked to the region encoding the tumour suppressor, a non-human
XX      transgenic eukaryote lacking a functional CAR-1 gene, a non-human
XX      non-transgenic eukaryote that over-expresses CAR-1 as compared to a similar
XX      anti-tumour activity by contacting a cell lacking functional CAR-1
XX      polypeptide, with a candidate substance and determining the effect of the
XX      candidate substance on the cell, an anti-tumour composition produced by
XX      contacting a cell lacking functional CAR-1 polypeptide, with a candidate
XX      substance, determining the effect of the candidate substance on the cell,
XX      identifying a candidate inhibitor substance, and making a composition and
XX      an isolated and purified nucleic acid that hybridizes, under high
XX      stringency conditions, to a DNA segment comprising about 15-3826 bases
XX      of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer,
XX      for altering the phenotype of a tumour cell, for treating cancers (e.g.,
XX      cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
XX      intestine, blood cells, colon, stomach, breast, endometrium, prostate,
XX      testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
XX      other tissues), and as a diagnostic or prognostic indicator of cancer.
XX      CAR-1 may also be used in screening compounds for activity in either
XX      stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking
XX      the effect of mutant CAR-1 molecule. The gene for CAR-1 is located
XX      on chromosome 1 (1p31-1p36). The present sequence is a BAC
XX      (bacterial artificial chromosome) containing part of the CAR-1 gene.
XX
XX
XX      Sequence 30676 BP; 7591 A; 7621 C; 7888 G; 6944 T; 632 other:
XX
XX
XX      Query Match      60.3%; Score 2308.6; DB 24; Length 30676;
XX      Best Local Similarity 98.7%; Pred. No. 0;
XX      Matches 2348; Conservative 0; Mismatches 29; Indels 2; Gaps 2;
XX
XX      1429 GGCCCTGCGAGTACACATCTGGAAGTCCCTGTTCAGAGATCCACCCAGTCCAGCC 1488

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Db 23371 GGTCCACAGCCTTCTCCCACTATCTTCTCTCCCTCCCAACCCCCACAGGCCAGGCC 23430
QY 1489 GCCCTAACCCCTGGACCCGGGACACAGCCACACAGCGCTGATCTGTGAGCACTGCAC 1548
Db 23431 GCCCTAACCCCTGGACCCGGGACACAGCCACACAGCGCTGATCTGTGAGCACTGCAC 23490
QY 1549 ATTGTGGCTTACGGCACTTGGACCCACAGCACTGCAAGACTGCGCAAAAGCGTTGCAT 1608
Db 23491 ATTGTGGCTTACGGCACTTGGACCCACAGCACTGCAAGACTGCGCAAAAGCGTTGCAT 23550
QY 1609 GTGGAGGTGTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1668
Db 23551 GTGGAGGTGTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 23610
QY 1669 GTGGTGGCGGAGAAAGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1728
Db 23611 GTGGTGGCGGAGAAAGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 23669
QY 1729 GGCAGCATCCAGTCCAGCCAGCCGCGGCTTCTACTGCACTGATGACAGTGGCAAC 1788
Db 23670 GGCAGCATCCAGTCCAGCCAGCCGCGGCTTCTACTGCACTGATGACAGTGGCAAC 23729
QY 1789 CAGTACAGGCGCTGACAGAGAGCCCTGGAGCGGCTTAAAGTCCGGGACAAAGCTTGAAC 1848
Db 23730 CAGTACAGGCGCTGACAGAGAGCCCTGGAGCGGCTTAAAGTCCGGGACAAAGCTTGAAC 23789
QY 1849 GTGGGTGTCTTCCTGGACTATGACCAAGCGTTCATCTTACAAATGCTATGACATG 1908
Db 23790 GTGGGTGTCTTCCTGGACTATGACCAAGCGTTCATCTTACAAATGCTATGACATG 23849
QY 1909 TCTGTGCTTACACCTTCGCGAGAAATGTCCTGGCAAGCTGCTCTTACTTACAGCCCT 1968
Db 23850 TCTGTGCTTACACCTTCGCGAGAAATGTCCTGGCAAGCTGCTCTTACTTACAGCCCT 23909
QY 1969 GGCACAGCGCAGCCCAATGGCAAGCTTCAAGCCCTGGGATGCAACACCGTCCGATC 2028
Db 23910 GGCACAGCGCAGCCCAATGGCAAGCTTCAAGCCCTGGGATGCAACACCGTCCGATC 23969
QY 2029 TAGTCCAGGCGAAGAGACACACACCTCTGGGACCACTGCGCACTGCAAGAGCCCTGC 2088
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QY 2089 CCAGGAAGATAGAAAGACTGAGACTCCAGCCACCGTGGCCACTGAGAGACTCAGGCCAGT 2148
Db 24030 CCAGG - AGATAGAAAGACTGAGACTCCAGCCACCGTGGCCACTGAGAGACTCAGGCCAGT 24088
QY 2149 TGTTCACCTCCAGCCTCCAGTCTGTAATAATGAGGTGGATTCCTACTTCTTAAACTC 2208
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QY 2209 TCTTCACGATCATGTTCTGTGATGCTGACCTTGAATAGGATACAGCTTGTATCCAAAG 2268
Db 24149 TCTTCACGATCATGTTCTGTGATGCTGACCTTGAATAGGATACAGCTTGTATCCAAAG 24208
QY 2269 ATGTGACATGAGCTTCTCTCAGGCAACCCCTGCCCAACCCCTCATCCCATCTTCTCAGG 2328
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QY 2329 GGCAGGGAAGTCTCTCAGGTCTCTCCAGGCCCAAGCCCTGACCTCAAGAAAGTGTCAAG 2388
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QY 2389 AGCATGCGCAGTATGTTGGAGCCCGAAGACACAGACACCTCTTATATGCCATGGCCT 2448
Db 24329 AGCATGCGCAGTATGTTGGAGCCCGAAGACACAGACACCTCTTATATGCCATGGCCT 24388
QY 2449 AAGACTTACCCCTGACCAAGCTATGATGAGGCGCATTTACCTTGAACCCCGAGTCCACAGTG 2508
Db 24389 AAGACTTACCCCTGACCAAGCTATGATGAGGCGCATTTACCTTGAACCCCGAGTCCACAGTG 24448
QY 2509 GTCACAGGTATGTCAGGTCTAGGGTTGCTGAGGCCAACTCTCTTCCACCCCCAC 2568
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Db 24449 GTCACAGGTATGTCAGGTCTAGGGTTGCTGAGGCCAACTCTCTTCCACCCCCAC 24508
QY 2569 ACCAAGAACTATATGTTGCTTCTTCTCCACTGATCTGCTGGTCAAGTATGATGCTG 2628
Db 24509 ACCAAGAACTATATGTTGCTTCTTCTTCTCCACTGATCTGCTGGTCAAGTATGATGCTG 24568
QY 2629 GCTGTGGAAGGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2688
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QY 2689 TGGCCACAGGCCCAAGGACAGAGGATGAGGATGATGATGATGATGATGATGATGATGATG 2748
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QY 3169 ACTGCAGAACTAGGCTCCCTCTGACAGGTCGCTGCCAGCAATATGATGCTGAGGCT 3228
Db 25109 ACTGCAGAACTAGGCTCCCTCTGACAGGTCGCTGCCAGCAATATGATGCTGAGGCT 25168
QY 3229 GCCCTCTCCACTTCACTACAGTCCCAATCTTAAATTTTAAAGAGATTTCTGTTGGG 3288
Db 25169 GCCCTCTCCACTTCACTACAGTCCCAATCTTAAATTTTAAAGAGATTTCTGTTGGG 25228
QY 3289 GGAACCTTAAATCAGATCCAGAACTTGGCTGCAAGGAGTCTGGAAATGTCAATTCCT 3348
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QY 3349 AGAAGGAATTAAGGTGGTGGAGCAAGCCCACTGCTGTTTTTTCACACAGATCCAA 3408
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Db 25409 ATCCCTGCCAGAGTGGGAACTGAGAGATGGGCTCAAGACTGAGACCTTAAATGTCTCC 25468
QY 3529 CCGGCTTGACTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3588
Db 25469 CCGGCTTGACTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 25528
QY 3589 CAACACACCTCCCAAGTACCGGGAAGAACTTAAACACAGGGGTTCTTAAATGTGCTGC 3648
Db 25529 CAACACACCTCCCAAGTACCGGGAAGAACTTAAACACAGGGGTTCTTAAATGTGCTGC 25588
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QY 3649 CCGGCGACCGGGGCTCCCTGGGCAANAAGATTTGTACGCCCTACCCCAACCTTCAA 3708
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QY 3769 TTATGATCAATTTGTATTAATTAAGTTACAGATGTCA 3807
DB 25709 TTATGATCAATTTGTATTAATTAAGTTACAGATGTCA 25747
RESULT 6
AAK80625
ID AAK80625 standard; DNA; 5866 BP.
XX AAK80625;
AC
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:35437.
XX
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KV cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PM WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
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 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-02595678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI: 2001-483426/52.
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure: SEQ ID NO 35437; 3071bp + Sequence Listing: English.
 XX
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 XX Sequence 5866 BP; 1464 A; 1580 C; 1489 G; 1333 T; 0 other;
 SO
 Query Match 60.3%; Score 2306.2; DB 22; Length 5866;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2330; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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 |||||||
 Db CCACACTGAGAGTGTGTGGCGGAGAGACCAAGTGGGTATCGGGCTGGCACACGA 240
 QY 1713 AGCCGCAAGCCGCAAGGAGACATCCAGATCCAGCCAGCCGCGGCTTCTACTGATCGT 1772
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 Db AGCCGCAAGCCGCAAGGAGACATCCAGATCCAGCCAGCCGCGGCTTCTACTGATCGT 299
 QY 1773 GATGCAAGATGGCAACCATAGACAGCGCTGCAGCGAGCCCTGGAGCGGCTTAAGCTCG 1832
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 Db GATGCAAGATGGCAACCATAGACAGCGCTGCAGCGAGCCCTGGAGCGGCTTAAGCTCG 359
 QY 1833 GGACAAAGCTTGACAAAGTGGGTGCTCTCTGACATGACCAAGGCTTCTCATCTTCTA 1892
 |||||||
 Db GGACAAAGCTTGACAAAGTGGGTGCTCTCTGACATGACCAAGGCTTCTCATCTTCTA 419
 QY 1893 CAATGCTGATGACATCTCTGCTCTACACCTTCCGCGAAGTTCCTGGCAAGCTCG 1952
 |||||||
 Db CAATGCTGATGACATCTCTGCTCTACACCTTCCGCGAAGTTCCTGGCAAGCTCG 479
 QY 1953 CTCTTACTTCAGCCCTGGCCAGACAGCCCAATGGCAAGAACTTCAGCCGCTGGGAT 2012
 |||||||
 Db CTCTTACTTCAGCCCTGGCCAGACAGCCCAATGGCAAGAACTTCAGCCGCTGGGAT 539
 QY 2013 CAACACCGTCCGATCTAGTCCAGGCAAGAGACACAACTTCTGGGACCACTGCCA 2072
 |||||||
 Db CAACACCGTCCGATCTAGTCCAGGCAAGAGACACAACTTCTGGGACCACTGCCA 599
 QY 2073 CCTGCAAGAGCCCTGGCCAGAAATGAAAGACCTGATCCAGCCACCGTGGCACTG 2132
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 Db CCTGCAAGAGCCCTGGCCAGAAATGAAAGACCTGATCCAGCCACCGTGGCACTG 658
 QY 2133 GAGACCTCAGGCGAGTGGTGTACCTCCAGCCCTCCAGTGTGTAATGGAGTGGATTC 2192
 |||||||
 Db GAGACCTCAGGCGAGTGGTGTACCTCCAGCCCTCCAGTGTGTAATGGAGTGGATTC 718
 QY 2193 CCTACTTCTTAACCTCTCCAGCATGATGTTCTGTAGCTGACTGTGATGAGGATA 2252
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 QY 2253 CAGCTTGTATCCAAAGATGTGACATGCTTCTCTCAAGGCAACCCCTGCCACCTCA 2312
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 QY 2313 TCCCAATCTTCTCAGGAGGAGGAGTACCTCCAGTGTCTCCAGGCCAGCCCTGA 2372
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 QY 2373 CCTCAGGAAGTGTCAAGAGCATGGCAGTAGTGGCAGCCGGAAGACACACACACCTTC 2432
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 Db CCTCAGGAAGTGTCAAGAGCATGGCAGTAGTGGCAGCCGGAAGACACACACACCTTC 958
 QY 2433 TTATGTCCATGGCTCAAGACTTAACCTTGACCAAGCTAGTGGCCATTTACCTTGG 2492
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 Db TTATGTCCATGGCTCAAGACTTAACCTTGACCAAGCTAGTGGCCATTTACCTTGG 1018
 QY 2493 ACCCGATCCACAGTGTGTACAGTAGTACCTGCTAGGCTTGGCTGAGACCAACT 2552
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 Db ACCCGATCCACAGTGTGTGTACAGTAGTACCTGCTAGGCTTGGCTGAGACCAACT 1078
 QY 2553 CTCTGCGACCCCGACACCAAGAACTATGTTCTTACTTCTCCCACTATGTGGTGT 2612
 |||||||
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 QY 2613 CAGTGTATGATGCTGTGGGCTGTGGAAAGCACTGTGATGTTGATCCACATTAATAGTCA 2672
 |||||||
 Db CAGTGTATGATGCTGTGGGCTGTGGAAAGCACTGTGATGTTGATCCACATTAATAGTCA 1198
 QY 2673 TGTGCAACCACTTCTCTGCGACAGGCGGAGGAGGAGGATGAGGATATACCAAACTGA 2732
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 Db TGTGCAACCACTTCTCTGCGACAGGCGGAGGAGGAGGATGAGGATATACCAAACTGA 1258

QY 2733 TGCAGAGCCCATTTGCTTAAAGCACTGCAGCAAGCTCCCTGCATGATCGAGTCC 2792
 DB 1259 TGCAGAGCCCATTTGCTTAAAGCACTGCAGCAAGCTCCCTGCATGATCGAGTCC 1318
 QY 2793 CCAGTACCTCTGACAAAGAGTCCAGCCCAACCTCTTACAGCAGGCTCTGACCTGCTA 2852
 DB 1319 CCACTACCTCTGACAAAGAGTCCAGCCCAACCTCTTACAGCAGGCTCTGACCTGCTA 1378
 QY 2853 GGGTGCAGAGGCTTTCAGAAAGCAGTGTGTAATTAGAGCCCAAGCACTGGAGGGCT 2912
 DB 1379 GGGTGCAGAGGCTTTCAGAAAGCAGTGTGTAATTAGAGCCCAAGCACTGGAGGGCT 1438
 QY 2913 GTTGGCTAGAGCCCTTGTGACAGCTGGCATATCTCAGTTAGATCTGCTGCAAGAAA 2972
 DB 1439 GTTGGCTAGAGCCCTTGTGACAGCTGGCATATCTCAGTTAGATCTGCTGCAAGAAA 1498
 QY 2973 CAAGAGCCACTTGTAGCTGGTTTAAATTAGCAAGATTTACTACCTGGCCCTGGTGGCT 3032
 DB 1499 CAAGAGCCACTTGTAGCTGGTTTAAATTAGCAAGATTTACTACCTGGCCCTGGTGGCT 1558
 QY 3033 TGCAGAAATTTGTGAGAGAGCTGAGAAAGCAGACTCTGCTGAATTTCCAGAACTCCAGC 3092
 DB 1559 TGCAGAAATTTGTGAGAGAGCTGAGAAAGCAGACTCTGCTGAATTTCCAGAACTCCAGC 1618
 QY 3093 GCCAGATTCATCATGTCTGTTGTGACCAAGAAAGCTGCCCATCTGACAGAGCCACTA 3152
 DB 1619 GCCAGATTCATCATGTCTGTTGTGACCAAGAAAGCTGCCCATCTGACAGAGCCACTA 1678
 QY 3153 TGCCAGAAAGCTGCTGACTGAGAACTAGGCTCCCTGCGCAGGCTCGTCCAGCCACT 3212
 DB 1679 TGCCAGAAAGCTGCTGACTGAGAACTAGGCTCCCTGCGCAGGCTCGTCCAGCCACT 1738
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 DB 1739 AGATGTCCTGAGGCTGCTCCCTCTCCACTTCACTCAGTGTCCCAATCTAAATTTTACA 1798
 QY 3273 AGAGATTCGTGTTGGGGAACTTAAGTCAGATCCAGAACTTGCTGCTGCAAGGGAGTCTGG 3332
 DB 1799 AGAGATTCGTGTTGGGGAACTTAAGTCAGATCCAGAACTTGCTGCTGCAAGGGAGTCTGG 1858
 QY 3333 GAAATGTCATTTCCCTAGAAAGAGTAAAGGTGGGTGGAGAGCAAGCCCACTGCGTGTCT 3392
 DB 1859 GAAATGTCATTTCCCTAGAAAGAGTAAAGGTGGGTGGAGAGCAAGCCCACTGCGTGTCT 1918
 QY 3393 CTGCCACAGCATCAATCTGTGAGAGACTCGGGAGGGGTGGAGTCCACATCTAGGGTGT 3452
 DB 1919 CTGCCACAGCATCAATCTGTGAGAGACTCGGGAGGGGTGGAGTCCACATCTAGGGTGT 1978
 QY 3453 CTTGCCCCCTTGGCTCTATCCCTGCGCAGAGGTGGGAACTGGAGAGTGGGCTGCAAGACT 3512
 DB 1979 CTTGCCCCCTTGGCTCTATCCCTGCGCAGAGGTGGGAACTGGAGAGTGGGCTGCAAGACT 2038
 QY 3513 GAGGCTAAATGTCTCCCGGCTTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3572
 DB 2039 GAGGCTAAATGTCTCCCGGCTTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2098
 QY 3573 CTTGGGGTCTCTGAC 3632
 DB 2099 CTTGGGGTCTCTGAC 2158
 QY 3633 TTTCTTAAATGGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGG 3692
 DB 2159 TTTCTTAAATGGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGG 2218
 QY 3693 TACCCCAACCTTCACTACAGAGATCTGGGCAACCCAGCAGATTTTAAATG 3752
 DB 2219 TACCCCAACCTTCACTACAGAGATCTGGGCAACCCAGCAGATTTTAAATG 2278
 QY 3753 TTGCCCCATTTTATGAGTATGATCAATTTTATTTAAATTTAAAGTTACAGATGCA 3807
 DB 2279 TTGCCCCATTTTATGAGTATGATCAATTTTATTTAAATTTAAAGTTACAGATGCA 2333

RESULT 7
 ABR12808
 ID ABR12808 standard; DNA; 30625 BP.
 XX
 AC ABR12808;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human tumour suppressor CAR-1, BAC clone 392H05 3' sequence.
 KW
 KW Human; ds; tumour suppressor; CAR-1; cytosolic; cancer; tumour;
 KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
 KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
 KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
 KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
 KW bacteria artificial chromosome; chromosome 1p31-1p36.
 XX
 OS Homo sapiens.
 XX
 PN WO200212285-A2.
 XX
 PD 14-FEB-2002.
 XX
 XX 09-AUG-2001; 2001WO-US25269.
 PE
 XX 10-AUG-2000; 2000US-225033P.
 PR 23-AUG-2000; 2000US-227560P.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX
 XX Killary A, Chandler D, Lott S;
 XI
 DR WPI; 2002-269088/31.
 XX
 XX New tumour suppressor CAR-1 polypeptides and polynucleotides, useful for
 PT diagnosing cancer, for altering the phenotype of a tumour cell, for
 PT treating cancers or as a diagnostic or prognostic indicator of cancer
 PT
 PT
 XX
 PS
 XX Disclosure; Page 149-157; 185bp; English.
 CC
 CC The invention relates to an isolated polynucleotide encoding a
 CC polypeptide being tumour suppressor, CAR-1. Also included are
 CC fragments of the polynucleotide from 15-500 nucleotides, fragments of
 CC the protein from 10-50 amino acids, an expression cassette comprising the
 CC polynucleotide under the control of a promoter operable in eukaryotic
 CC cells, a method for suppressing growth of a cancer cells by contacting
 CC the cells with the expression cassette (i.e. gene therapy), a cell
 CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody, a hybridoma cell that produces the monoclonal
 CC antibody, a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1, or by
 CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC non-transgenic eukaryote, a method of screening a candidate substance for
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases
 CC of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer,
 CC for altering the phenotype of a tumour cell, for treating cancers (e.g.,
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or

CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking
CC the effect of mutant CAR-1 molecule. The gene for CAR-1 is located
CC on chromosome 1 (1p31-1p36). The present sequence is a BAC
CC (bacterial artificial chromosome) containing part of the CAR-1 gene.
XX

Sequence 30625 BP; 8084 A; 7712 C; 7487 G; 7314 T; 28 other:

Query Match 58.9%; Score 2252.8; DB 24; Length 30625;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 57; Indels 3; Gaps 3;

QY 1429 GGGCCCCCTGACATACACATCTGGAGTCCCTGTTCCAGAGACATCCACCAGTGGCAGCC 1488
DB 21906 GGTTCACACACCTTCTCCACATCTCTCTCCCTCCCAACCCCAAGGCCAGCC 21965
QY 1489 GCCCTAACCCCTGACCCGGGACAGCCCAAGCCGCTGATCCTGTCGAGCGCTGACCC 1548
DB 21966 GCCCTAACCCCTGACCCGGGACAGCCCAAGCCGCTGATCCTGTCGAGCGCTGACCC 22025
QY 1549 ATTGTGGCTTACGGCACTTGGACCCACAGCCACTGACAGACTGCGCAAGCGCTTCGAT 1608
DB 22026 ATTGTGGCTTACGGCACTTGGACCCACAGCCACTGACAGACTGCGCAAGCGCTTCGAT 22085
QY 1609 GTGGAGGTGTCGCTGCTGGCTTGTGAAGCTTTCAGTATGTCGCTCCACTACTGGAGGTG 1668
DB 22086 GTGGAGGTGTCGCTGCTGGCTTGTGAAGCTTTCAGTATGTCGCTCCACTACTGGAGGTG 22145
QY 1669 GTGGAGGTGTCGCTGCTGGCTTGTGAAGCTTTCAGTATGTCGCTCCACTACTGGAGGTG 1728
DB 22146 GTGGAGGTGTCGCTGCTGGCTTGTGAAGCTTTCAGTATGTCGCTCCACTACTGGAGGTG 22205
QY 1729 GGCAGCATCCAGATCCAGCCACGCGGCTTCTACTGATGCTGTATGACAGATGGCAAC 1788
DB 22206 GGCAGCATCCAGATCCAGCCACGCGGCTTCTACTGATGCTGTATGACAGATGGCAAC 22265
QY 1789 CAGTACAGCGCTGCGACGAGCCCTGAGCGGCTTACGTCGCGGACAAAGCTTGAACAA 1848
DB 22266 CAGTACAGCGCTGCGACGAGCCCTGAGCGGCTTACGTCGCGGACAAAGCTTGAACAA 22325
QY 1849 GTGGGTGTCTCTGAGCTATGACCAAGGCTTGTCTATCTTACAAATGCTGATGACATG 1908
DB 22326 GTGGGTGTCTCTGAGCTATGACCAAGGCTTGTCTATCTTACAAATGCTGATGACATG 22385
QY 1909 TCCTGGCTCTACACCTTCCGCGAGAACTTCCCTGGAGACTGCTGCTTACTTACAGCCCT 1968
DB 22386 TCCTGGCTCTACACCTTCCGCGAGAACTTCCCTGGAGACTGCTGCTTACTTACAGCCCT 22445
QY 1969 GGCAGAGCGCCAGCAATGGCAAGAGCTTCAAGCCCTGCGATCAACACCGTCCGATC 2028
DB 22446 GGCAGAGCGCCAGCAATGGCAAGAGCTTCAAGCCCTGCGATCAACACCGTCCGATC 22505
QY 2029 TAGTCCAGGACAGAGAGACCAACCTCCTGGAGACATGCGACCTGGAAGAGCCCTGC 2088
DB 22506 TAGTCCAGGACAGAGAGACCAACCTCCTGGAGACATGCGACCTGGAAGAGCCCTGC 22564
QY 2089 CCAGAGAGATAGAAAGCTGGAAGCTGAGCCCAAGCTGCGGCACTGAGAGCTCAGGCGAGT 2148
DB 22565 CCAGG-AGATAGAAAGAGCTGGAAGCTGAGCCCAAGCTGCGGCACTGAGAGCTCAGGCGAGT 22623
QY 2149 TGTTTTACCTCCAGCTCCAGCTGCTGTAATAATGAGAGTTGCATTTCTTCTTAACATC 2208
DB 22624 TGTTTTACCTCCAGCTCCAGCTGCTGTAATAATGAGAGTTGCATTTCTTCTTAACATC 22683
QY 2209 TCTTCCAGGATGATGTTCTGTAGCTGACCTGATAGGAGTACAGCTTGTATGCAAGG 2268
DB 22684 TCTTCCAGGATGATGTTCTGTAGCTGACCTGATAGGAGTACAGCTTGTATGCAAGG 22743
QY 2269 ATGTGACATGCTTCTCTCAGGAGCAACCCCTGCGCAACCCCTATCCCATCTTCTCAGG 2328
DB 22744 ATGTGACATGCTTCTCTCAGGAGCAACCCCTGCGCAACCCCTATCCCATCTTCTCAGG 22803

QY 2329 GGCAGGAGACTACCTTCCAGTGTCTCCCTCCACGCCCAAGCCCTGACTCAGGAAGTGTAG 2388
DB 22804 GGCAGGAGACTACCTTCCAGTGTCTCCCTCCACGCCCAAGCCCTGACTCAGGAAGTGTAG 22863
QY 2389 AGCATGGCAAGTATGTTGGGAGCCCGAAGACACAGACACCCCTTATGTCCTATGGCCCT 2448
DB 22864 AGCATGGCAAGTATGTTGGGAGCCCGAAGACACAGACACCCCTTATGTCCTATGGCCCT 22923
QY 2449 AAGACTTACCCCTGACCAAGCTAGTATGAGGACCTTATACCTTGAACCCCAAGTCCACAGTG 2508
DB 22924 AAGACTTACCCCTGACCAAGCTAGTATGAGGACCTTATACCTTGAACCCCAAGTCCACAGTG 22983
QY 2509 GTTCACAGTATGTAACCTGCTTACAGGTTGCTGTCGTCGAGACCAACCTCTCTCCACCCCAC 2568
DB 22984 GTTCACAGTATGTAACCTGCTTACAGGTTGCTGTCGTCGAGACCAACCTCTCTCCACCCCAC 23043
QY 2569 ACCAAGACTATATGTTGCTTCTTCTTCTCCACAGTATGCTGCTGCTGATGATGCTGTG 2628
DB 23044 ACCAAGACTATATGTTGCTTCTTCTTCTCCACAGTATGCTGCTGCTGATGATGCTGTG 23103
QY 2629 GCCTGTGGAAGGCACTGTGATGTTGATGTCACACATTTATATGTCATGTCACACCTTCC 2688
DB 23104 GCCTGTGGAAGGCACTGTGATGTTGATGTCACACATTTATATGTCATGTCACACCTTCC 23163
QY 2689 TGCCCAAGGCGGAGGAGCAAGGTTGAGGTTATACCAAAAGCTGATGCAAGCCCATTAGC 2748
DB 23164 TGCCCAAGGCGGAGGAGCAAGGTTGAGGTTATACCAAAAGCTGATGCAAGCCCATTAGC 23223
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DB 23464 GCTGTGTTAATTAAGCAAGATTTACTACTGCGCCCTGCTGCTGCTTGCATAAATTTGTGGA 23523
QY 3048 AGAGCTGGAAGACAGACTGCTGTAATTTCCAGAACTCCAGCGCCAGATTCATCATG 3107
DB 23524 AGAGCTGGAAGACAGACTGCTGTAATTTCCAGAACTCCAGCGCCAGATTCATCATG 23583
QY 3108 TGTGTTGTGACAGGAAGCTGCCCCATCTGAGGAAGGCACTATGCGCAAGAAAGCTGCT 3167
DB 23584 TGTGTTGTGACAGGAAGCTGCCCCATCTGAGGAAGGCACTATGCGCAAGAAAGCTGCT 23643
QY 3168 GACTGCAAGACTAGGCTCCCTGCGCAAGGTTCCGTCGCAAGCAATAGATTCCTGAGGCC 3227
DB 23644 GACTGCAAGACTAGGCTCCCTGCGCAAGGTTCCGTCGCAAGCAATAGATTCCTGAGGCC 23703
QY 3228 TGCCCTCTTCCCACTTCACTCAGTTCCTCAATATTAATTTTACAAAGATTTGTTGG 3287
DB 23704 TGCCCTCTTCCCACTTCACTCAGTTCCTCAATATTAATTTTACAAAGATTTGTTGG 23763
QY 3288 GGGAACTTAAGTACAGATCCAGACCTTGGCTGGAAGGAGTGGGAAATGCTATTTCC 3347
DB 23764 GGGAACTTAAGTACAGATCCAGACCTTGGCTGGAAGGAGTGGGAAATGCTATTTCC 23823
QY 3348 TAGAAGAGTTAGGTTGGTTGGTGAAGCAAGCCCACTGCGTCTTTTGTGCAACAGATCA 3407
DB 23824 TAGAAGAGTTAGGTTGGTTGGTGAAGCAAGCCCACTGCGTCTTTTGTGCAACAGATCA 23883
QY 3408 ATCTGTAAGAACTCGGGAAGAGGTTGATGCACATCTAAGGTTGTCTGCTGCTTGGCTC 3467


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Db      23884 ATCGGAAAACTCGGAGAGGCTGAGTCCACATCTAGAGGTGTCTCCCTCGCCCTGCGTC 23943
OY      3468 TATCCCTCCAGAGCTGGGAACTGGAGAGTGGCTCGACAGCTGAGCCTTAATGTC 3527
Db      23944 TATCCCTCCAGAGCTGGGAACTGGAGAGTGGCTCGACAGCCTTAATGTC 24003
OY      3528 CCGGCGCTTGACTTTCTTTCTAGTCTGGGGCCAGATTCGCACTTGGGCTCTGAC 3587
Db      24004 CCGGCGCTTGACTTTCTTTCTAGTCTGGGGCCAGATTCGCACTTGGGCTCTGAC 24063
OY      3588 ACAACACACATCCCAAGTAGCCCGAAGAGCTAAACACAGGGGCTTCTTAATGCGTC 3647
Db      24064 ACAACACACATCCCAAGTAGCCCGAAGAGCTAAACACAGGGGCTTCTTAATGCGTC 24123
OY      3648 CCCCCGACCCGGGCTTCCTTGGGCAAAAGAAATTCACGCCCTACCCCAACCTTCA 3707
Db      24124 CCCCCGACCCGGGCTTCCTTGGGCAAAAGAAATTCACGCCCTACCCCAACCTTCA 24183
OY      3708 ACTACCAAGATCTGGCGCCACCCAGCAGTATTTTATTTAAATGTTGCCATTTATGA 3767
Db      24184 ACTACCAAGATCTGGCGCCACCCAGCAGTATTTTATTTAAATGTTGCCATTTATGA 24243
OY      3768 GTATGATCAATTTGTATTAATTTAACTTACAGATGTCA 3807
Db      24244 GTATGATCAATTTGTATTAATTTAACTTACAGATGTCA 24283
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AAK80626
ID      AAK80626 standard; DNA; 5858 BP.
XX
AC      AAK80626;
XX
DT      07-NOV-2001 (first entry)
XX
DE      Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:35438.
XX
KW      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cystostatic; gene therapy; vaccine; metastasis; ds.
OS      Homo sapiens.
XX
FN      MO200157182-A2.
PD      09-AUG-2001.
XX
PE      17-JAN-2001; 2001WO-US01354.
XX
PR      31-JAN-2000; 2000US-0179065.
PR      04-FEB-2000; 2000US-0180628.
PR      02-MAR-2000; 2000US-0184664.
PR      16-MAR-2000; 2000US-0186350.
PR      17-MAR-2000; 2000US-0189874.
PR      18-APR-2000; 2000US-0190076.
PR      19-MAY-2000; 2000US-0198123.
PR      07-JUN-2000; 2000US-0205515.
PR      28-JUN-2000; 2000US-0209467.
PR      30-JUN-2000; 2000US-0214886.
PR      07-JUL-2000; 2000US-0215135.
PR      07-JUL-2000; 2000US-0216647.
PR      11-JUL-2000; 2000US-0216880.
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PR      14-AUG-2000; 2000US-0225213.
PR      14-AUG-2000; 2000US-0225214.
PR      14-AUG-2000; 2000US-0225266.
PR      14-AUG-2000; 2000US-0225267.
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PR      14-AUG-2000; 2000US-0225268.
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PR      14-AUG-2000; 2000US-0225757.
PR      14-AUG-2000; 2000US-0225758.
PR      14-AUG-2000; 2000US-0225759.
PR      22-AUG-2000; 2000US-0226279.
PR      22-AUG-2000; 2000US-0226681.
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PR      23-AUG-2000; 2000US-0227182.
PR      30-AUG-2000; 2000US-0228924.
PR      01-SEP-2000; 2000US-0228287.
PR      01-SEP-2000; 2000US-0229343.
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PR      05-SEP-2000; 2000US-0229509.
PR      06-SEP-2000; 2000US-0229513.
PR      06-SEP-2000; 2000US-0230437.
PR      06-SEP-2000; 2000US-0230438.
PR      08-SEP-2000; 2000US-0231242.
PR      08-SEP-2000; 2000US-0231243.
PR      08-SEP-2000; 2000US-0231244.
PR      08-SEP-2000; 2000US-0231413.
PR      08-SEP-2000; 2000US-0231414.
PR      08-SEP-2000; 2000US-0232080.
PR      08-SEP-2000; 2000US-0232081.
PR      12-SEP-2000; 2000US-0231968.
PR      14-SEP-2000; 2000US-0233397.
PR      14-SEP-2000; 2000US-0233398.
PR      14-SEP-2000; 2000US-0233399.
PR      14-SEP-2000; 2000US-0234000.
PR      14-SEP-2000; 2000US-0234001.
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PR      21-SEP-2000; 2000US-0234223.
PR      21-SEP-2000; 2000US-0234274.
PR      25-SEP-2000; 2000US-0234997.
PR      25-SEP-2000; 2000US-0234998.
PR      26-SEP-2000; 2000US-0235484.
PR      27-SEP-2000; 2000US-0235834.
PR      27-SEP-2000; 2000US-0235835.
PR      29-SEP-2000; 2000US-0236327.
PR      29-SEP-2000; 2000US-0236367.
PR      29-SEP-2000; 2000US-0236368.
PR      29-SEP-2000; 2000US-0236369.
PR      02-OCT-2000; 2000US-0236370.
PR      02-OCT-2000; 2000US-0236802.
PR      02-OCT-2000; 2000US-0237037.
PR      02-OCT-2000; 2000US-0237038.
PR      02-OCT-2000; 2000US-0237039.
PR      02-OCT-2000; 2000US-0237040.
PR      13-OCT-2000; 2000US-0239935.
PR      13-OCT-2000; 2000US-0239937.
PR      20-OCT-2000; 2000US-0240960.
PR      20-OCT-2000; 2000US-0241221.
PR      20-OCT-2000; 2000US-0241785.
PR      20-OCT-2000; 2000US-0241786.
PR      20-OCT-2000; 2000US-0241787.
PR      20-OCT-2000; 2000US-0241808.
PR      20-OCT-2000; 2000US-0241809.
PR      01-NOV-2000; 2000US-0241826.
PR      08-NOV-2000; 2000US-0244617.
PR      08-NOV-2000; 2000US-0246475.
PR      08-NOV-2000; 2000US-0246476.
PR      08-NOV-2000; 2000US-0246477.
PR      08-NOV-2000; 2000US-0246478.
PR      08-NOV-2000; 2000US-0246523.
PR      08-NOV-2000; 2000US-0246524.
PR      08-NOV-2000; 2000US-0246525.
PR      08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000: 2000US-0246527.
 PR 08-NOV-2000: 2000US-0246528.
 PR 08-NOV-2000: 2000US-0246532.
 PR 08-NOV-2000: 2000US-0246609.
 PR 08-NOV-2000: 2000US-0246610.
 PR 08-NOV-2000: 2000US-0246611.
 PR 08-NOV-2000: 2000US-0246613.
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 PR 17-NOV-2000: 2000US-0249211.
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 PR 17-NOV-2000: 2000US-0249216.
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 PR 17-NOV-2000: 2000US-0249244.
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 PR 17-NOV-2000: 2000US-0249264.
 PR 17-NOV-2000: 2000US-0249265.
 PR 17-NOV-2000: 2000US-0249297.
 PR 17-NOV-2000: 2000US-0249299.
 PR 17-NOV-2000: 2000US-0249300.
 PR 01-DEC-2000: 2000US-0250160.
 PR 01-DEC-2000: 2000US-0250391.
 PR 05-DEC-2000: 2000US-0251030.
 PR 05-DEC-2000: 2000US-0251988.
 PR 05-DEC-2000: 2000US-0256179.
 PR 06-DEC-2000: 2000US-0251479.
 PR 08-DEC-2000: 2000US-0251856.
 PR 08-DEC-2000: 2000US-0251868.
 PR 08-DEC-2000: 2000US-0251869.
 PR 08-DEC-2000: 2000US-0251889.
 PR 08-DEC-2000: 2000US-0251890.
 PR 11-DEC-2000: 2000US-0254097.
 PR 05-JAN-2001: 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 PS
 XX Disclosure; SEQ ID NO 35438; 3071pp + Sequence Listing; English.
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SO Sequence 5858 BP; 1481 A; 1575 C; 1462 G; 1340 T; 0 other;

Query Match

58.9%; Score 2252; DB 22; Length 5858;

Best Local Similarity 98.6%; Pred. No. 0;
 Matches 2303; Conservative 0; Mismatches 30; Indels 3; Gaps 3;
 QY 1473 CCACCCGTCGCGCCGCCCTTAACCCCTGGAGCCGGGACAGCCACAGCCGCTGATCCT 1532
 Db 1 CCCACAGTCCAGCCGCCCTTAACCCCTGGAGCCGGGACAGCCACAGCCGCTGATCCT 60
 QY 1533 GTGGAGAGTGCACCATTTGTGGCTTACGGCAACTTGACCAAGCCATGCAAGACTC 1592
 Db 61 GTGGAGAGTGCACCATTTGTGGCTTACGGCAACTTGACCAAGCCATGCAAGACTC 120
 QY 1593 GCCAAAGCGTTGATGTGAGAGTGTGGTGTCTGAGGCTTCAAGCTTCAATGTGGCCT 1652
 Db 121 GCCAAAGCGTTGATGTGAGAGTGTGGTGTCTGAGGCTTCAAGCTTCAATGTGGCCT 180
 QY 1653 CCACCTAGTGGAGGTGTGGTGTGGGAGAGACCACTGGGTGATGGGGTGGACACGA 1712
 Db 181 CCACCTAGTGGAGGTGTGGTGTGGGAGAGACCACTGGGTGATGGGGTGGACACGA 240
 QY 1713 AGCCGCAAGCCGCAAGGGCAGCATCCAGATCCAGCCAGCCGGCTTCTACTGATCGT 1772
 Db 241 AGCCGCAAGCCGCAAGGGCAGCATCCAGATCCAGCCAGCCGGCTTCTACTGATCGT 300
 QY 1773 GATGCAAGATGCAACGATGACAGCGCTTGCAGGAGCCCTGGAGCGGCTTAACTCGC 1832
 Db 301 GATGCAAGATGCAACGATGACAGCGCTTGCAGGAGCCCTGGAGCGGCTTAACTCGC 360
 QY 1833 GGACAAAGCTTGACAAAGGTGGGTGCTCTCGAGCTATGACCAAGGCTTGCTACTCTA 1892
 Db 361 GGACAAAGCTTGACAAAGGTGGGTGCTCTCGAGCTATGACCAAGGCTTGCTACTCTA 420
 QY 1893 CAATGCTGATGACATGCTGCTGCTCTACACCTTCCGGAGAAAGTTCCCTGGCAAGCTCG 1952
 Db 421 CAATGCTGATGACATGCTGCTGCTCTACACCTTCCGGAGAAAGTTCCCTGGCAAGCTCG 480
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 QY 2073 CTGCAAGAGCCCTGCGCAGAGAAAGTAAAGACCTGATCCAGCCAGCCGCTGCACTG 2132
 Db 600 CTGCAAGAGCCCTGCGCAGAG - AGATGAAACCTGATCCAGCCAGCCGCTGCACTG 658
 QY 2133 GAGACCTCAGAGCCAGTGTGTACCTCCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTC 2192
 Db 659 GAGACCTCAGAGCCAGTGTGTACCTCCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTC 718
 QY 2193 CCTACTTCTTAACCTCTCTCCAGCATGATGTTCTAGCTGATGATGATGATGATGATGATG 2252
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 QY 2253 CAGTTTGTATCAGAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2312
 Db 779 CAGTTTGTATCAGAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 838
 QY 2313 TCCCATCTTCTCAGGGGACAGGGGACCTTCCAGTGTCTCCTCCAGCCAGCCCTGGA 2372
 Db 839 TCCCATCTTCTCAGGGGACAGGGGACCTTCCAGTGTCTCCTCCAGCCAGCCCTGGA 898
 QY 2373 CCTGAGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2432
 Db 899 CCTGAGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
 QY 2433 TTATGTCCATGAGCTTAAGATTAAGCTTACCCCTGACCAAGTATGATGATGATGATGATGATG 2492
 Db 959 TTATGTCCATGAGCTTAAGATTAAGCTTACCCCTGACCAAGTATGATGATGATGATGATG 1018
 QY 2493 ACCCCAGTCCACAGTGTGACAGGTAGTACCTGATGATGATGATGATGATGATGATGATG 2552
 Db 2552 ACCCCAGTCCACAGTGTGACAGGTAGTACCTGATGATGATGATGATGATGATGATGATG

CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases
CC of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer,
CC for altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking
CC the effect of mutant CAR-1 molecule. The gene for CAR-1 is located
CC on chromosome 1 (1p31-1p36). The present sequence is a BAC
CC (bacterial artificial chromosome) containing part of the CAR-1 gene.
XX

Sequence 45845 BP; 12103 A; 10668 C; 10633 G; 12441 T; 0 other:

Query Match 26.0%; Score 995.8; DB 24; Length 45845;
Best Local Similarity 99.7%; Pred. No. 3e-181;
Matches 1008; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 24164 AGGCTGCGTGGAGCGGAGGCGTGGCTGCTAGCTCGCGGGGGTAAAGGGTGGCGGGG 24223
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DB 24224 CCAGGGTTTGGGGCCGGGATCCGGCAGCTGAGCGGGGCGGACCCCTCTCTCTGCGC 24283
QY 121 GGCACAGGCAATGATACGGCTGCGCTGCGTGGCCCTCCCTCCAGATTTCCCATGCCCA 180
DB 24284 GGCACAGGCAATGATACGGCTGCGCTGCGTGGCCCTCCCTCCAGATTTCCCATGCCCA 24343
QY 181 GCTTCTGCGCTCCCGACACGCGCCACCCCGGATTTGAGACCCCTTAAAGGGCTGCAC 240
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DB 24524 TTGAGCTGGCCATACCTAGACTGCGCTCCCGGGGTGCGTCCAGAGTCTAGGC 24583
QY 421 GCGCACCCTTCTCGCGTTACCTCTCTCCGAGACAGACCCCTCTCTCCGAGTGC 480
DB 24584 GCGCACCCTTCTCGCGTTACCTCTCTCCGAGACAGACCCCTCTCTCCGAGTGC 24643
QY 481 TCGTACCCCTGCTGCGGGGCTGCTGCGGGGCCAGGCCCTGCGTCTCCGACA 540
DB 24644 TCGTACCCCTGCTGCGGGGCTGCTGCGGGGCCAGGCCCTGCGTCTCCGACA 24703
QY 541 GCGCACCCTTCTCGCGTTACCTCTCTCCGAGACAGACCCCTCTCTCCGAGTGC 600
DB 24704 GCGCACCCTTCTCGCGTTACCTCTCTCCGAGACAGACCCCTCTCTCCGAGTGC 24762
QY 601 GCCATGGCGTGAAGCTCAAGAGAGAGAGTCTGCTCATCTGCTGAGACATCTACAG 660
DB 24763 GCCATGGCGTGAAGCTCAAGAGAGAGAGTCTGCTCATCTGCTGAGACATCTACAG 24822
QY 661 GACCGGCTGAGCTGGGCTGCGAGCACTATTCTGCGCGCGCTGCACTACAGGAGACTGG 720
DB 720 GACCGGCTGAGCTGGGCTGCGAGCACTATTCTGCGCGCGCTGCACTACAGGAGACTGG 720

DB 24823 GACCGGCTGAGCTGGGCTGCGAGCACTATTCTGCGCGCGCTGCACTACAGGAGACTGG 24882
QY 721 GTCGCGAGAGAGGCGAGGCGCGCCGAGTGCCTCCGAGTGGCGGCGCAGCTTGCAGG 780
DB 24883 GTCGCGAGAGAGGCGAGGCGCGCCGAGTGCCTCCGAGTGGCGGCGCAGCTTGCAGG 24942
QY 781 CCCGCGTGGCGCCACCTCAAGCTGGCCAACTGCTGAGAGCGCTTACAGCTCTTCCG 840
DB 24943 CCCGCGTGGCGCCACCTCAAGCTGGCCAACTGCTGAGAGCGCTTACAGCTCTTCCG 25002
QY 841 CTGAGCGCATCTCAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
DB 25003 CTGAGCGCATCTCAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25062
QY 901 AACCTTCTGCTCAGCAGCAGCGCGCTTCTGCTTCTTCTGCGAGCGCTGACTG 960
DB 25063 AACCTTCTGCTCAGCAGCAGCGCGCTTCTGCTTCTTCTGCGAGCGCTGACTG 25122
QY 961 CACGAGCAGCATGAGTCAACCGGCGAGCAGCGCGCTTCAAGCAGCTGAG 1011
DB 25123 CACGAGCAGCATGAGTCAACCGGCGAGCAGCGCGCTTCAAGCAGCTGAG 25173

RESULT 10
ABK12807
ID ABK12807 standard; DNA; 49744 BP.

XX ABK12807;
XX 18-JUN-2002 (first entry)
XX Human tumour suppressor CAR-1, BAC clone 392H05 5' sequence.

XX Human: ds: tumour suppressor; CAR-1; cytostatic; cancer; tumour;
XX gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
XX colon cancer; stomach cancer; breast cancer; endometrial cancer;
XX prostate cancer; testicular cancer; ovarian cancer; skin cancer;
XX head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
XX bacteria artificial chromosome; chromosome 1p31-1p36.

XX Homo sapiens.
XX WO200212285-A2.
XX 14-FEB-2002.
XX 09-AUG-2001; 2001MO-US25269.

XX 10-AUG-2000; 2000US-225033P.
XX 23-AUG-2000; 2000US-227560P.
XX (TEXA) UNIV TEXAS SYSTEM.

XX Killary A, Chandler D, Lott S;
XX WPI; 2002-269088/31.

XX New tumour suppressor CAR-1 polypeptides and polynucleotides, useful for
XX diagnosing cancer, for altering the phenotype of a tumour cell, for
XX treating cancers or as a diagnostic or prognostic indicator of cancer
XX

XX Disclosure; Page 135-148; 185pp; English.

XX The invention relates to an isolated polynucleotide encoding a
XX polypeptide being tumour suppressor, CAR-1. Also included are
XX fragments of the polynucleotide from 15-5000 nucleotides, fragments of
XX the protein from 10-50 amino acids, an expression cassette comprising the
XX polynucleotide under the control of a promoter operable in eukaryotic
XX cells, a method for suppressing growth of a cancer cells by contacting
XX the cells with the expression cassette (i.e. gene therapy), a cell
XX comprising the expression cassette, an anti-CAR-1 monoclonal or
XX polyclonal antibody, a hybridoma cell that produces the monoclonal

Db 333 TGACAAGGTTGGTGTCTTCTGACTATGACCAAGGCTTGCATCTTCTACATGCTGA 274
 Qy 1902 TGACATGTCCTGGCTCTACACCTTCCGGAGAAATTCCTGGCAAGCTTGTCTTACTT 1961
 Db 273 TGACATGTCCTGGCTCTACACCTTCCGGAGAAATTCCTGGCAAGCTTGTCTTACTT 214
 Qy 1962 CAGCCCTGGCCAGACCAAGCAATGGCAAGAAAGCTTCAAGCCGCTGGGATTAACACGCT 2021
 Db 213 CAGCCCTGGCCAGACCAAGCAATGGCAAGAAAGCTTCAAGCCGCTGGGATTAACACGCT 154
 Qy 2022 CCGCATCTAGTCCAGCAGAAAGAGACCAACCTCTGGAGCACTGCACTGCACTGCAAGA 2081
 Db 153 CCGCATCTAGTCCAGCAGAAAGAGACCAACCTCTGGAGCACTGCACTGCACTGCAAGA 94
 Qy 2082 GCCCTGCCAGAGAAATGAAAGCTGATCTCAGCCCAAGCTGGCCACTGGAGACCTCA 2141
 Db 93 GCCCTGCCAGAG-AGATGAAAGAACTGATCTCAGCCCAAGCTGGCCACTGGAGACCTCA 35
 Qy 2142 GGCCAGTTGTTTACCTCCAGCCTCCAGCTGTA 2175
 Db 34 GGCCAGTTGTTTACCTCCAGCCTCCAGCTGTA 1
 RESULT 13
 ID ABA28765/C
 ID ABA28765 standard; DNA; 573 Bp.
 AC ABA28765;
 XX
 DT 23-JAN-2002 (first entry)
 DE Probe #7231 for gene expression analysis in human heart cell sample.
 XX
 KW Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 OS Homo sapiens.
 XX
 PM WO200157274-A2.
 XX
 PD 09-AUG-2001.
 XX
 PE 30-JAN-2001; 2001WO-US00666.
 XX
 PF 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0633366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SC, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 XX
 PS Claim 1; SEQ ID NO 7231; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 CC
 SQ Sequence 573 Bp; 109 A; 164 C; 179 G; 121 T; 0 other;
 Query Match 14.7%; Score 562; DB 22; Length 573;
 Best Local Similarity 99.8%; Pred. No. 26-98;
 Matches 573; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1602 CTTGATGAGGAGTGTGCGGTCTGGGTTCTAAGCCTTCAATAGGCGTCACTACTG 1661
 Db 573 CTTGATGAGGAGTGTGCGGTCTGGGTTCTAAGCCTTCAATAGGCGTCACTACTG 514
 Qy 1662 GAGAGTGTGTGGGAGAAAGCAAGTGGTGTATCGGGCTGGCAGCAAGAGCGCAAG 1721
 Db 513 GAGAGTGTGTGGGAGAAAGCAAGTGGTGTATCGGGCTGGCAGCAAGAGCGCAAG 454
 Qy 1722 CCGCAAGGGCAGCATTCAGATCCAGCCAGCCGCGCTTCTATCGATCGATGACAGCA 1781
 Db 453 CCGCAAGGGCAGCATTCAGATCCAGCCAGCCGCGCTTCTATCGATCGATGACAGCA 394
 Qy 1782 TGGCAACCACTACAGCGCTGCAAGGAGCGCTGGAAGCGGCTTAACGTCCGGAGACGT 1841
 Db 393 TGGCAACCACTACAGCGCTGCAAGGAGCGCTGGAAGCGGCTTAACGTCCGGAGACGT 334
 Qy 1842 TGACAAGGTGGTGTCTTCTGACTATGACCAAGGCTTGTCTATCTTCAATGCTGA 1901
 Db 333 TGACAAGGTGGTGTCTTCTGACTATGACCAAGGCTTGTCTATCTTCAATGCTGA 274
 Qy 1902 TGACATGTCCTGGCTCTACACCTTCCGGAGAAATTCCTGGCAAGCTTGTCTTACTT 1961
 Db 273 TGACATGTCCTGGCTCTACACCTTCCGGAGAAATTCCTGGCAAGCTTGTCTTACTT 214
 Qy 1962 CAGCCCTGGCCAGACCAAGCAATGGCAAGAAAGCTTCAAGCCGCTGGGATTAACACGCT 2021
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 Qy 2022 CCGCATCTAGTCCAGCAGAAAGAGACCAACCTCTGGAGCACTGCACTGCACTGCAAGA 2081
 Db 153 CCGCATCTAGTCCAGCAGAAAGAGACCAACCTCTGGAGCACTGCACTGCACTGCAAGA 94
 Qy 2082 GCCCTGCCAGAGAAATGAAAGCTGATCTCAGCCCAAGCTGGCCACTGGAGACCTCA 2141
 Db 93 GCCCTGCCAGAG-AGATGAAAGAACTGATCTCAGCCCAAGCTGGCCACTGGAGACCTCA 35
 Qy 2142 GGCCAGTTGTTTACCTCCAGCCTCCAGCTGTA 2175
 Db 34 GGCCAGTTGTTTACCTCCAGCCTCCAGCTGTA 1
 RESULT 14
 ID AAK08953/C
 ID AAK08953 standard; DNA; 573 Bp.
 AC AAK08953;
 XX
 DT 05-NOV-2001 (first entry)
 DE Human brain expressed single exon probe SEQ ID NO: 8944.
 XX
 KW Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer; ss.
 OS Homo sapiens.
 XX
 PM WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00667.
 XX

OY 1902 TGACATGTCCTGCTCTACACCTTCGCGAGAGATTCCCTGGCAAGCTCTGCTTACTT 1961
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Db 273 TGACATGTCCTGCTCTACACCTTCGCGAGAGATTCCCTGGCAAGCTCTGCTTACTT 214
1963 CAGCCCTGGCCAGAGCCAGCCAAATGGCAAGCTTCAGCCGCTCCGGATCAACACCGT 2021
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Db 213 CAGCCCTGGCCAGAGCCAGCCAAATGGCAAGCTTCAGCCGCTCCGGATCAACACCGT 154
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Db 93 GCCCTGCCAGG-AGATAGAAAGACCTGGACTCCAGCCCAACCGTGGCCACTGGAGACTCA 35
OY 2142 GGCCAGTTGTTTACCTCCAGCCTCCAGTCTGTA 2175
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Db 34 GGCCAGTTGTTTACCTCCAGCCTCCAGTCTGTA 1

Search completed: October 8, 2003, 15:19:18
Job time : 966 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 15:20:54 ; Search time 7436 Seconds

(without alignments)
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Title: US-09-927-091-3

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Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
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9: gb_est1:*
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22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*
29: gb_gss82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	878.2	23.0	1049	12	BM457033
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3	780.6	20.4	935	13	B0069145
4	761.6	19.9	973	13	B0879837

5	743.8	19.4	781	14	CB956370	CB956370 AGENCOURT
6	730.8	19.1	769	14	CA444761	CA444761 UI-H-DH1-
7	727.4	19.0	931	13	B0527114	B0527114 AGENCOURT
8	701.8	18.3	906	13	B0171407	B0171407 AGENCOURT
9	699.8	18.3	983	10	BE795637	BE795637 601590620
10	697	18.2	2726	11	AK048725	AK048725 Mus muscu
11	696.4	18.2	785	14	CB960090	CB960090 AGENCOURT
12	695.4	18.2	851	10	BC703589	BC703589 602686426
13	690.2	18.0	768	9	AL554421	AL554421
14	662.4	17.3	664	12	BM722392	BM722392 UI-E-EO-
15	657.4	17.2	922	14	CA984031	CA984031 AGENCOURT
16	654.2	17.1	682	14	CA309985	CA309985 UI-H-FTI-
17	645.2	16.9	766	13	B0612412	B0612412 UI-M-EMO-
18	634	16.6	634	12	B0018441	B0018441 UI-H-DH1-
19	632	16.5	632	12	BM994555	BM994555 UI-H-DHO-
20	632	16.5	633	12	BM994326	BM994326 UI-H-DHO-
21	600.2	15.7	762	12	BM946923	BM946923 UI-M-ERDP
22	592.2	15.5	628	9	A0132503	A0132503
23	587	15.3	776	13	B0121855	B0121855 603147035
24	578.8	15.1	1018	13	B0723205	B0723205 AGENCOURT
25	568.2	14.9	661	13	B0611033	B0611033 UI-M-FCO-
26	565.6	14.8	823	13	B0214796	B0214796 603757509
27	563.8	14.7	732	9	AL554364	AL554364
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29	547.4	14.3	705	10	BE258134	BE258134 601114755
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31	534.8	14.0	790	13	B0117232	B0117232 603002550
32	531.2	13.9	893	13	B0412532	B0412532 603154826
33	529.2	13.8	543	9	AM070327	AM070327
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35	520.4	13.6	557	9	A0154016	A0154016
36	519	13.6	519	9	AL138362	AL138362 DKEP2762P
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45	488	12.8	501	13	B0187235	B0187235 UI-E-EJ1-

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cdna clone IMAGE:5583269
5', mRNA sequence.
ACCESSION
BM457033
VERSION
BM457033.1 GI:18506073
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1049)
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM2346 row: b column: 06
High quality sequence stop: 671.

FEATURES
SOURCE

Location/Qualifiers
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/db_xref="taxon:9606"
/mol_type="mRNA"
/clone="IMAGE:5583269"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

BASE COUNT 246 a 298 c 262 g 239 t 4 others
ORIGIN

Query Match 23.0%; Score 878.2; DB 12; Length 1049;
Best Local Similarity 99.4%; Pred. No. 2.8e-127;
Matches 902; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 2386 CAGAGCATGGCCAGTAGTTGGCAGCCCGAAGACACACAGCACACCTCTTATGTCCTCAG 2445
DB 1 CAGAGCATGGCCAGTAGTTGGCAGCCCGAAGACACACAGCACACCTCTTATGTCCTCAG 60
QY 2446 CCTAAGACTTACCCCTGACCAAGCTAGTGGGCGCATTTACCTTGACCCAGTCCACA 2505
DB 61 CCTAAGACTTACCCCTGACCAAGCTAGTGGGCGCATTTACCTTGACCCAGTCCACA 120
QY 2506 GTGGTCACAGTAGTACCTGTGCTCTAGAGGTTGCTGAGAGGCAACCTCTCTGCGCACCC 2565
DB 121 GTGGTCACAGTAGTACCTGTGCTCTAGAGGTTGCTGAGAGGCAACCTCTCTGCGCACCC 180
QY 2566 CACACCAAGAACTATATGGTCTCTACTCTCCACTGATCTGTGGTCAGATGATGATCT 2625
DB 181 CACACCAAGAACTATATGGTCTCTACTCTCCACTGATCTGTGGTCAGATGATGATCT 240
QY 2626 GTGGCCTGTGGAAGGCAAGCCTGTGTTGATGTCACACATTTATGTCATGTCGACACCT 2685
DB 241 GTGGCCTGTGGAAGGCAAGCCTGTGTTGATGTCACACATTTATGTCATGTCGACACCT 300
QY 2686 TCCCTGCCACAGGCGGAGGAGGAGGATATACCAAGCTGATGACAGAGCCATT 2745
DB 301 TCCCTGCCACAGGCGGAGGAGGAGGATATACCAAGCTGATGACAGAGCCATT 360
QY 2746 AGCCTAAAGCACTGCAGACAAAGCCTCCCTGATGATGATGATGATGATGATGATGAT 2805
DB 361 AGCCTAAAGCACTGCAGACAAAGCCTCCCTGATGATGATGATGATGATGATGATGATGAT 420
QY 2806 ACAAGAGTCCAGCAAGCCTCTTGCAGAGGCTCTGTGACCTGTAGGGTGCAGAGAGC 2865
DB 421 ACAAGAGTCCAGCAAGCCTCTTGCAGAGGCTCTGTGACCTGTAGGGTGCAGAGAGC 480
QY 2866 TTCCAGAGAGAGTGTGTATTTAGAGCAACCAAGCACTGGAGGAGGCTTTGGTATGAGCC 2925
DB 481 TTCCAGAGAGAGTGTGTATTTAGAGCAACCAAGCACTGGAGGAGGCTTTGGTATGAGCC 540
QY 2926 CTGTGCAAGTGGCATCTATCTCATGTTAGAGATCCTGCTGCAGAAACAGAGCCACTTG 2985
DB 541 CTGTGCAAGTGGCATCTATCTCATGTTAGAGATCCTGCTGCAGAAACAGAGCCACTTG 600
QY 2986 TAGCTGTTTATTTATGACAGGATTTTACTACTGGCCCTGTGGCTTGCAAAATTGTG 3045
DB 601 TAGCTGTTTATTTATGACAGGATTTTACTACTGGCCCTGTGGCTTGCAAAATTGTG 660
QY 3046 GAAGAGTGGAGAGAGAGACTCTGCTGAATTTCCAGAACTCCAGAGGCCAGATTCA 3105
DB 661 GAAGAGTGGAGAGAGAGACTCTGCTGAATTTCCAGAACTCCAGAGGCCAGATTCA 720
QY 3106 TGTCTGTTGTGACAGAGAAAGCTGCCCCCATCTGCAGAGAAAGCACTATGCGAGAAAGCTG 3165
DB 721 TGTCTGTTGTGACAGAGAAAGCTGCCCCCATCTGCAGAGAAAGCACTATGCGAGAAAGCTG 780

QY 3166 CTGATGCGAGAACTAGGCT-CCCTTGGCCAGGTCCTGCGCACGCCAATAGATGTCCTGAG 3224
DB 781 CTGATGCGAGAACTAGGCTCCCTCTGCGCAGGTCCTGCGCACGCCAATAGATGTCCTGAG 840
QY 3225 GCGTCCCGCTCTCCACTTTCAGTCACTGAGTCCCAATCTAAA-TTTTACAAGAGATTCTGT 3283
DB 841 GCGTCCCGCTCTCCACTTTCAGTCACTGAGTCCCAATCTAAA-TTTTACAAGAGATTCTGT 900
QY 3284 TTGGGGG 3290
DB 901 TTTGGGG 907

RESULT 2
CA310925/C
LOCUS
DEFINITION UI-CF-FNO-afb-j-06-0-UI-s1 UI-CF-FNO Homo sapiens cDNA clone
UI-CF-FNO-afb-j-06-0-UI 3', mRNA sequence.
ACCESSION CA310925
VERSION CA310925.1 GI:24529023
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 835)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
SOURCE

Location/Qualifiers
1. 835
/organism="Homo sapiens"
/db_xref="taxon:9606"
/mol_type="mRNA"
/clone="UI-CF-FNO-afb-j-06-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human Lung epithelial cell libraries (EN1 and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_Lib-UI-CF-FNO
TAG-TISSUE-Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_SEQ-CTGCTCAGCT"

BASE COUNT 201 a 197 c 219 g 216 t 2 others
ORIGIN

Query Match 20.7%; Score 793.4; DB 14; Length 835;

Best Local Similarity 99.3%; Pred. No. 5e-114; Matches 827; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 2992 GTTAAATGACAGGATTTACTACTGCCCCCTGGTGGCTTCAAAATGTTGAAGAG 3051
 Db 830 GTTAAATGACAGAGG-ATTACTACTGCCCCCTGGT-CTTCAAAATGNNTTGAGAG 773
 QY 3052 CTGGAGAGACAGACTCTGTGTAATTTTCAGGAAGCTCCAGCGCCAGATTCATCATCTCTG 3111
 Db 772 CTGGAGAGACAGACTCTGTG-ATTTCAGGAAGCTCCAGCGCCAGATTCATCATCTCTG 714
 QY 3112 TTGTGACAGGAAGCTGCCCCCATCTGCAAGAGCCATATGCCAGAAAGCTGCTGACT 3171
 Db 713 TTGTGACAGGAAGCTGCCCCCATCTGCAAGAGCCATATGCCAGAAAGCTGCTGACT 654
 QY 3172 GCAGACTAGAGCTCCCTGTCAGAGGTCGTCGAGCAATATATGTCGAGAGGCTGTC 3231
 Db 653 GCAGACTAGAGCTCCCTGTCAGAGGTCGTCGAGCAATATATGTCGAGAGGCTGTC 594
 QY 3232 CCTCTCCACTCTCACTCACTGTCCTCCAAATCTAAATTTTACAGAGATTCGTTGGGGGA 3291
 Db 593 CCTCTCCACTCTCACTCACTGTCCTCCAAATCTAAATTTTACAGAGATTCGTTGGGGGA 534
 QY 3292 ACTTAAGTACAGATCCAGAACTTGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGA 3351
 Db 533 ACTTAAGTACAGATCCAGAACTTGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGA 474
 QY 3352 AGGAAGTTAGGGTGGTGAGAGCAAGCCCACTGCTTTTTCGCCACAGCATCATCATG 3411
 Db 473 AGGAAGTTAGGGTGGTGAGAGCAAGCCCACTGCTTTTTCGCCACAGCATCATCATG 414
 QY 3412 TGAAGAATCGGAGAGGTTGAGTCCACATCTAGAGTTCCTGCTGCTGCTGCTATC 3471
 Db 413 TGAAGAATCGGAGAGGTTGAGTCCACATCTAGAGTTCCTGCTGCTGCTGCTATC 354
 QY 3472 CCTGCCCAAGAGTGGGAACTGGAGAGTGGCTGCAAGACTGAGCTTAATGTCCTCCCG 3531
 Db 353 CCTGCCCAAGAGTGGGAACTGGAGAGTGGCTGCAAGACTGAGCTTAATGTCCTCCCG 294
 QY 3532 GCCTTACTTTTCTTCTAGTCTGCTGGGCTTATGATCTGCACTTGGGGTCTGACAGAA 3591
 Db 293 GCCTTACTTTTCTTCTAGTCTGCTGGGCTTATGATCTGCACTTGGGGTCTGACAGAA 234
 QY 3592 CACACCATCCCAAGTAGCCGGAAGCTAAACACAGGGGGTCTTAAATGCTGCTGCC 3651
 Db 233 CACACCATCCCAAGTAGCCGGAAGCTAAACACAGGGGGTCTTAAATGCTGCTGCC 174
 QY 3652 CGCCACCGGGCTCCTTGGGCAAAAGATTTGTAGCCCTACCCCACTTCAACTA 3711
 Db 173 CGCCACCGGGCTCCTTGGGCAAAAGATTTGTAGCCCTACCCCACTTCAACTA 114
 QY 3712 CCAGAACTTGGGCAAGAGTATTTTATTTAAATGTTGCCATTTTGAAGTTA 3771
 Db 113 CCAGAACTTGGGCAAGAGTATTTTATTTAAATGTTGCCATTTTGAAGTTA 54
 QY 3772 TGATCAATTTGATTAATTAATTAAGTATGATGTCAAAAAA 3824
 Db 53 TGATCAATTTGATTAATTAATTAAGTATGATGTCAAAAAA 1

RESULT 3
 LOCUS B0069145 935 bp mRNA linear EST 02-APR-2002
 DEFINITION AGENCOURT 6738796 NIH_MGC_47 Homo sapiens cdna clone IMAGE:5803435
 5', mRNA sequence.
 ACCESSION B0069145
 VERSION B0069145.1 GI:19898191
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 935)

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LICM2039 row: 9 column: 20
 High quality sequence stop: 708.
 Location/Qualifiers
 1. 935
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5803435"
 /tissue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_47"
 /note="Organ: Brain; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald H. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 200 a 305 c 244 g 186 t

ORIGIN

Query Match 20.4%; Score 780.6; DB 13; Length 935;
 Best Local Similarity 98.4%; Pred. No. 4.7e-112;
 Matches 820; Conservative 0; Mismatches 9; Indels 4; Gaps 3;

QY 1618 TCGGTCTGGGCTCTCAAGCTTCAGTAGGGGCTCAGTACAGAGTGGAGTGGTGGG 1677
 Db 1 TCGGTCTGGGCTCTCAAGCTTCAGTAGGGGCTCAGTACAGAGTGGAGTGGTGGG 60
 QY 1678 GAGAAAGCCAGTGGTGTATCGGGTGGCAACAGAGCCGCAAGGCGACATC 1737
 Db 61 GAGAAAGCCAGTGGTGTATCGGGTGGCAACAGAGCCGCAAGGCGACATC 120
 QY 1738 CAGATCAGCCAGCCGCGGCTTCTACTGATCTGTATGACAGATGGCAACAGTACAGC 1797
 Db 121 CAGATCAGCCAGCCGCGGCTTCTACTGATCTGTATGACAGATGGCAACAGTACAGC 180
 QY 1798 GCCTGAGAGGAGCCGTGAGCGGGCTTAAGTCCGGAGCAAGTTACAAAGTGGTGTG 1857
 Db 181 GCCTGAGAGGAGCCGTGAGCGGGCTTAAGTCCGGAGCAAGTTACAAAGTGGTGTG 240
 QY 1858 TTCTGTGACTATGACCAAGGCTTGTCTATCTTACAAATGCTATGATATGCTCTGGCTC 1917
 Db 241 TTCTGTGACTATGACCAAGGCTTGTCTATCTTACAAATGCTATGATATGCTCTGGCTC 300
 QY 1918 TACACCTTCGCGAGAGTTCCTGCGAAGCTCTCTTACTTACAGCCCTGGCAGAGC 1977
 Db 301 TACACCTTCGCGAGAGTTCCTGCGAAGCTCTCTTACTTACAGCCCTGGCAGAGC 360
 QY 1978 CACGCCAATGGCAAGAGCTTACGCGCGTGGATCAACACCGCTCCGCAATCTGTCCAGG 2037
 Db 361 CACGCCAATGGCAAGAGCTTACGCGCGTGGATCAACACCGCTCCGCAATCTGTCCAGG 420
 QY 2038 CAGAAGAGACCAACACTCTCTGGGACACTGCGACCTGCAAGAGCCCTCCAGAGA 2097
 Db 421 CAGAAGAGACCAACACTCTCTGGGACACTGCGACCTGCAAGAGCCCTCCAGAG-AGA 479
 QY 2098 TAGAAGACTGAGCTCCAGCCACCGTGGCAGTGGAGACTGAGACCTGATTTTACCC 2157
 |||||||

Db 480 TAGAAGACCTGGACTCCAGCCACCCTGGCCACTGGAGACTCAGAGCCAGTTGTTACCC 539

QY 2158 TCAGACCTCCAGTGTGTAAATGAGAGGTTCATTCCTACTTCTTAACTCTCTCCAGC 2217
|||||
Db 540 TCAGACCTCCAGTGTGTAAATGAGAGGTTCATTCCTACTTCTTAACTCTCTCCAGC 599

QY 2218 ATGATGTCCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCT 2277
|||||
Db 600 ATGATGTCCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCT 659

QY 2278 GGCTTCTCTCAGAGGAGCAACCCCTGAGCCCACTCATCTCTCTCAGAGGAGGGA 2337
660 GGCTTCTCTCAGAGGAGCAACCCCTGAGCCCACTCATCTCTCTCAGAGGAGGGA 719

QY 2338 CTACCTTCAGAGTGTCTCTCTCAGAGCCCACTCATCTCTCTCAGAGGAGTGTGAGCATGGCC 2397
720 CTACCTTCAGAGTGTCTCTCTCAGAGCCCACTCATCTCTCTCAGAGGAGTGTGAGCATGGCC 779

QY 2398 AGTA--GTGGCAGCCCGAAGACACAGCA--CCCTCTTATGTCTCCATGGCC 2447
780 AGTAAGTTGGAGCCCGAAGACACAGCA--CCCTCTTATGTCTCCATGGCC 832

RESULT 4
BO879837 973 bp mRNA linear EST 16-AUG-2002
LOCUS BO879837
DEFINITION AGENCOURT_821257 lupskl_dorsal_root_ganglion Homo sapiens cDNA
ACCESSION BO879837
VERSION BO879837
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 973)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: csapbs@email.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LRAM13568 row: e column: 23
High quality sequence start: 48
High quality sequence stop: 599.
Location/Qualifiers
1..973
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6182398"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="lupskl_dorsal_root_ganglion"
/note="Vector: PCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGGTCGG-3' and
5'-GACATGTCCTGATCGGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies"

BASE COUNT 209 a 329 c 236 g 199 t

ORIGIN

Query Match 19.9%; Score 761.6; DB 13; Length 973;
Best Local Similarity 95.8%; Pred. No. 4.3e-109;
Matches 858; Conservative 0; Mismatches 29; Indels 9; Gaps 7;

QY 1689 GTGGGTATCGGGCTGGCAGCAGAACCCGCAAGCGGCAAGGCGACATCCAGATCCAGCC 1748
|||
Db 10 GTCCGGATTTCTCCGGGATACAGAACCGCGCAAGCGGCAAGGCGACATCCAGATCCAGCC 69

QY 1749 CAGCGCGGGCTTCTACTGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1808
70 CAGCGCGGGCTTCTACTGATCGATGATGATGATGATGATGATGATGATGATGATGATGAT 129

QY 1809 GCCCTGAGCGGGCTTAACTCCGAGCAACCTGACAAAGGTGGGTGTCTCTCTGACTA 1868
130 GCCCTGAGCGGGCTTAACTCCGAGCAACCTGACAAAGGTGGGTGTCTCTCTGACTA 189

QY 1869 TGACCAAGGCTTGTCTCATCTCTTCAATGCTGATGACATGTCCTGGCTCTACACCTTCCG 1928
190 TGACCAAGGCTTGTCTCATCTCTTCAATGCTGATGACATGTCCTGGCTCTACACCTTCCG 249

QY 1929 CGAGAAGTTCCTGGCAAGCTCTGCTTACTTCAAGCCCTGGCCAGAGCCAGCCCAATGG 1988
250 CGAGAAGTTCCTGGCAAGCTCTGCTTACTTCAAGCCCTGGCCAGAGCCAGCCCAATGG 309

QY 1989 CAAGAACGTTGAGCGCGTGGCGATCAACACCGTCCGATCTAGTCCAGAGGAGAGAC 2048
310 CAAGAACGTTGAGCGCGTGGCGATCAACACCGTCCGATCTAGTCCAGAGGAGAGAC 369

QY 2049 CACAACCTCTCTGGGACACTCTCCACCTGCAAGAGCCCTGCCAGAGATGAAAGACCTG 2108
370 CACAACCTCTCTGGGACACTCTCCACCTGCAAGAGCCCTGCCAGAGATGAAAGACCTG 428

QY 2109 GACTTCAGACCCAGCGTGGCGACTGAGAGCTCAGAGCCAGTGTATACCTCCAGCTTCA 2168
429 GACTTCAGACCCAGCGTGGCGACTGAGAGCTCAGAGCCAGTGTATACCTCCAGCTTCA 488

QY 2169 GTCTGTAAATGAGAGTTCATCTCTCTTCTTAACTCTCTCTCTCTCTCTCTCTCTCTCT 2228
489 GTCTGTAAATGAGAGTTCATCTCTCTTCTTAACTCTCTCTCTCTCTCTCTCTCTCTCT 548

QY 2229 GTACTCTGACCTTGATGAGATACAGTTTGATTCAGAGATGACATGCTCTCTCTC 2268
549 GTACTCTGACCTTGATGAGATACAGTTTGATTCAGAGATGACATGCTCTCTCTC 608

QY 2289 AGGCAACCCCTGGCCAACTCTCATCCCATCTCTCTGAGGCGAGGAGACTACCTTCAG 2348
609 AGGCAACCCCTGGCCAACTCTCATCCCATCTCTCTGAGGCGAGGAGACTACCTTCAG 668

QY 2349 TGT-CTCCCTCAGAGCCCTGACCTCAGAGAGTGTCAAGAGAT-GGCCAGTAGTTGG 2406
669 TGTCTCTCTCAGAGCCCTGACCTCAGAGAGTGTCAAGAGATGAGGAGTGTAGTTGG 728

QY 2407 CAG-CCCGAAAGACACAGACAC-CTCTTATGTCCTCATGCTTAAAGCTTACCCCTG 2462
729 CAGCCCGGAAAGACACAGACACCTCTTATGTCCTCATGCTTAAAGCTTACCCCTG 788

QY 2463 ACCAAGCTAGTAGAGGAGGATTTACCTTGAAGCCAGAGTCCAGAGTGTGACATAGTAGTAC 2522
789 ACCAAGCTAGTAGAGGAGGATTTACCTTGAAGCCAGAGTGTGACATAGTAGTAC 848

QY 2523 CT-GGTCTTAGAGTGTCTCTGAGAGCAAC-CTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2576
849 CTGGGTCTTAGAGGAGTGTCTTAAACCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 904

RESULT 5
CB956370 781 bp mRNA linear EST 29-APR-2003
LOCUS CB956370
DEFINITION AGENCOURT_13666719 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30353395 5', mRNA sequence.

ACCESSION CB956370

VERSION CB956370.1 GI:30212487
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 781)
 AUTHORS NIH-MGC <http://mgi.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLOnTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LILN at:
<http://image.liln.gov>
 Plate: NDCM154 row: a column: 20
 High quality sequence stop: 582.
 Location/Qualifiers
 1..781
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30353395"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone.lib="NIH-MGC 184"
 /note="Organ: Pooled-Glandular: Vector: pDNR-LIB: Site_1:
 SfiI (ggccatcagcc); Site_2: SfiI (ggccgcctcgcc);
 Library is oligo-dT primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATAGGCG-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCCGAGCGGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech laboratories (Palo Alto,
 CA). Note: this is a NIH-MGC Library."
 BASE COUNT 191 a 205 c 202 g 181 t 2 others
 ORIGIN
 Query Match 19.4%; Score 743.8; DB 14; Length 781;
 Best Local Similarity 98.6%; Pred. No. 2.7e-106;
 Matches 770; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
 Oy 2583 GGTTCCTACTCTCCACTGATCTGCTGTCAGTATGCTGTGGCCTGTGAAGCA 2642
 |||||||
 Db 3 GGTTCCTACTCTCCACTGATCTGCTGTCAGTATGCTGTGGCCTGTGAAGCA 62
 |||||||
 Oy 2643 CCTGTACTAGTACACATTAATAGTCATGTCACACACTTCTCTGCCACAGCGCA 2702
 |||||||
 Db 63 CCTGTACTAGTACACATTAATAGTCATGTCACACACTTCTCTGCCACAGCGCA 122
 |||||||
 Oy 2703 GGGACAGGGTGGGTATACCAAGCTGATGCAGAGCCATTAGCTTAAAGCAACTGC 2762
 |||||||
 Db 123 GGGACAGGGTGGGTATACCAAGCTGATGCAGAGCCATTAGCTTAAAGCAACTGC 182
 |||||||
 Oy 2763 AGGACAACTCTCCCTGATGATGAGTCCCAAGTAGTCTGTAGAACAGAGTCCAGCAAC 2822
 |||||||
 Db 183 AGGACAACTCTCCCTGATGATGAGTCCCAAGTAGTCTGTAGAACAGAGTCCAGCAAC 242
 |||||||
 Oy 2883 CCTCTTACGACAGGCTCTGTGACTGCTAGAGGCTCAGAGAGCTTCCAGAACCACTTGT 2882
 |||||||
 Db 243 CCTCTTACGACAGGCTCTGTGACTGCTAGAGGCTCAGAGAGCTTCCAGAACCACTTGT 302
 |||||||
 Oy 2883 GTAATTAGACCAAGCACTGGAGAGGCTGTGGCTAGACCCCTTGCAGACTTGGCAT 2942
 |||||||
 Db 303 GTAATTAGACCAAGCACTGGAGAGGCTGTGGCTAGACCCCTTGCAGACTTGGCAT 362

Oy 2943 CTATCTCAGTAGATTCCTGCTGCAGAAAAAAGAGCCACTGTAGCTGGTTTAATTAGA 3002
 |||||||
 Db 363 CTATCTCAGTAGATTCCTGCTGCAGAAAAAAGAGCCACTGTAGCTGGTTTAATTAGA 422
 |||||||
 Oy 3003 CAAGATTTACTACCTGGCCCCCTGGTGGCTTGCAGAAATTTGTTGGAAGAGCTGGAGACGA 3062
 |||||||
 Db 423 CAAGATTTACTACCTGGCCCCCTGGTGGCTTGCAGAAATTTGTTGGAAGAGCTGGAGACGA 482
 |||||||
 Oy 3063 GACTGTGCAATTTCCAGGAAGTCCAGAGCCGAGATTCATGATCTGTGTGACACAGG 3122
 |||||||
 Db 483 GACTGTGCAATTTCCAGGAAGTCCAGAGCCGAGATTCATGATCTGTGTGACACAGG 542
 |||||||
 Oy 3123 AAAGTGGCCCCCATGTCAGAGAGCCACTATGCCAGAAAGCTGTGACTGCAGAACTAGG 3182
 |||||||
 Db 543 AAAGTGGCCCCCATGTCAGAGAGCCACTATGCCAGAAAGCTGTGACTGCAGAACTAGG 602
 |||||||
 Oy 3183 CTTCCCTGCGCACGGTCCGCTGGCCAGCCATATATGCTCGAGAGCCTGCCCTCTCCACT 3242
 |||||||
 Db 603 CTTCCCTGCGCACGGTCCGCTGGCCAGCCATATATGCTCGAGAGCCTGCCCTCTCT-CCACT 661
 |||||||
 Oy 3243 TCACTCAGTCCCAATCTAAATTTTACAGAGATTCGTTGGGGGAACCTTAAGTAG 3302
 |||||||
 Db 662 TCACTCAGT-CCAAATCTAAATTTTACAGAGATTCGTTGGGGGAACCTTAAGTAG 720
 |||||||
 Oy 3303 ATCCAGAACTTGGCTGCAAGGAGCTGGGAATGTCAATTCCTAGAGAGAACTTAGG 3362
 |||||||
 Db 721 ATCCAGAACTTGGCTGCAAGGAGCTGGGAATGTCAATTCCTAGAGAGAACTTAGG 780
 |||||||
 Oy 3363 G 3363
 Db 781 G 781

RESULT 6
 CA444761/c
 LOCUS CA444761 769 bp mRNA linear EST 08-NOV-2002
 DEFINITION UI-H-DH1-awv-f-12-0-UI-s1 NCI_CGAP-DH1 Homo sapiens cDNA clone
 UI-H-DH1-awv-f-12-0-UI 3', mRNA sequence.
 CA444761
 ACCESSION CA444761.1 GI:24809181
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 769)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA-yes.
 FEATURES
 source
 Location/Qualifiers
 1..769
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-DH1-awv-f-12-0-UI"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pRT73-Pac (Pharmacia) with a
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 NCI_CGAP-DH1 is a normalized cDNA library containing the

[illegible]

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		/lab_host="DH10B (phage-resistant)"	
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		/site_2="Salt; Cloned unidirectionally. Primer: Oligo dT.	
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Query Match	18.3%; Score 701.8; DB 13; Length 906;		
Best Local Similarity	94.2%; Pred. No. 9,2e-100;		
Matches 751:	Conservative 0; Mismatches 42; Indels 4; Gaps 2;		
QY	1983 CAATGCGAAGAACGTTCAGCCGGCTGGGGATCACACCGTCGCATCTAGTCCAGCAGA	2042	
Db	1 CAAATGGCAAGAACGTTTCAGCCGGCTGGGGATCACACCGTCGCATCTAGTCCAGCAGA	60	
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Db	300 CTCTCTCAGGGCAACCCCTGGCCCAACCTCATCCCCATCTTCTCAGGGGAGGGAGCTTACC	359	
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Db	480 GACACAGTATGATGGGCAATTTACCCCTTGACCCCAAGTCACAGATGGGCACAGATTAGTAC	539	
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Db	600 GGTTCCTACTCTTCTCCCACTGATCTGCTGGTGCAGTATGATGATCTGTGGCTGTGAAGCA	659	
QY	2643 CCTGGTATGTAGTGCCACACATTTATATGATGATGATGATGATGATGATGATGATGATGAT	2700	
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 DEFINITION 601590620F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944860 5',
 mRNA sequence.
 ACCESSION BE795637
 VERSION BE795637.1 GI:10216835
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 983)
 NIH-MGC http://mgs.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apds@email.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Inceye Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at: image.linl.gov
 Plate: LINC802 row: 9 column: 05
 High quality sequence stop: 791.
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 231 a 267 c 275 g 210 t
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 Query Match 18.3%; Score 699.8; DB 10; Length 983;
 Best Local Similarity 97.3%; Pred. No. 1.8e-99;
 Matches 787; Conservative 0; Mismatches 12; Indels 10; Gaps 7;
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 Oy 2628 GGCTGTGGAAGGACCTGTGATGATGATGATGATGATGATGATGATGATGATG 2687
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 181 CTGGCCACAGCGGAGGAGGAGGATGATGATGATGATGATGATGATGATGATG 240
 Oy 2748 CTTAAAGCAATGTCAGAGCAAGACCTCTCTGATGATGATGATGATGATGATGATG 2807
 241 CTTAAAGCAATGTCAGAGCAAGACCTCTCTGATGATGATGATGATGATGATGATG 300
 Oy 2808 AAGAGTCACCAACCTCTTTCAGCCAGGCTCTGTGATGATGATGATGATGATGATG 2867
 301 AAGAGTCACCAACCTCTTTCAGCCAGGCTCTGTGATGATGATGATGATGATGATG 360

Oy 2868 CCAGAACAGTGTGTGTAATTAGAGCCAGCACTGGGAGGGCTGTGTGACACCT 2927
 Db 361 CCAGAACAGTGTG-TGTAATTAGAGCCAGCACTGGGAGGGCTGTGTGACACCT 419
 Oy 2928 TGTGAGACTGGGATCTATCTCATGTTAGATCCCTGCTGCAGAAACAGGACCACTGTGA 2987
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 F15, CLONE NT2R3004617, WEAKLY SIMILAR TO ZINC-BINDING PROTEIN A33
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 AK048725
 ACCESSION AK048725.1 GI:26093070
 VERSION
 KEYWORDS HNC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 3
 Shibata, K., Itoh, M., Alzawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Ishii, K., Kikunishi, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL MEDLINE 20530913


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RESULT 11
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DEFINITION IMAGE:30340472 5', mRNA sequence.
ACCESSION CB960090
VERSION CB960090.1 GI:30216206
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

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JOURNAL
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: Dr. Stefan Hanson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (NIKEI)
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDA370 row: 9 column: 09
High quality sequence stop: 650.
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insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."
BASE COUNT 129 a 316 c 217 g 123 t
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Matches 697; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
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AUTHORS	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
COMMENT	On Feb 15, 2001 this sequence version replaced gi:12895186. Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqrel@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of				

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 QY 731 AGCGCAGAGGCGCGCGCGAGTGTGCGCGAGTGGCGGCGAGTGGCGGCGCGCGCGCG 790
 Db 421 AGCGCAGAGGCGCGCGCGAGTGTGCGCGAGTGGCGGCGAGTGGCGGCGCGCGCGCG 480
 QY 791 CGCCAGAGCTCAAGCTGCGCAACATGCTGAGAGCGCTACAGCTCCCTCCCGCTGAGCGCA 850
 Db 481 CGCCAGAGCTCAAGCTGCGCAACATGCTGAGAGCGCTACAGCTCCCTCCCGCTGAGCGCA 540
 QY 851 TCTCTCAAGCG 910
 Db 541 TCTCTCAAGCG 600
 QY 911 GCCTACAGGAGCGCGCGCTTCTGTGCTTCTGTGAGAGAGGAGCTGACAGAGAGAG 970
 Db 601 GCCTACAGGAGCGCGCGCTTCTGTGCTTCTGTGAGAGAGGAGCTGACAGAGAGAG 660
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 Db 661 ATCA 664
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 LOCUS AGENCOURT_11296524 NIH_MGC_164 Mus musculus cDNA clone
 DEFINITION IMAGE:30147594 5', mRNA sequence.
 ACCESSION CA984031
 VERSION CA984031.1 GI:27516685
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 922)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Dr. David Rowe and Dr. Mina
 cDNA Library Preparation: Invitrogen Corp
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM0065 row: b column: 19
 High quality sequence start: 17
 High quality sequence stop: 645.
 Location/Qualifiers
 1..922
 FEATURES
 source

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 /db_xref="taxon:10090"
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 /lab_host="DH10B (phage-resistant)"
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 /note="Vector: pCMV-SPORT6.1.cdb; Site_1: EcoRV; site_2:
 NotI; Non-normalized full-length enriched library from
 pooled mouse embryonic limb, maxilla and mandible, day
 10.5 and 11.5 (size selected for the 0.5-1 kb fragments)
 Cloned directionally, priming method: Oligo-dT. cDNA
 enrichment: >1k bp, Average insert size 1.8k bp. Priming
 sequence: 5' GACTAGTCTTGAATCGGAGCGGCGCCGCT 3'. Tissue
 contributed by, David Rowe. Library constructed by Resgen,
 Invitrogen Corp."
 BASE COUNT 211 a 286 c 262 g 163 t
 ORIGIN
 Query Match 17.2%; Score 657.4; DB 14; Length 922;
 Best Local Similarity 86.5%; Pred. No. 7.6e-93;
 Matches 772; Conservative 0; Mismatches 116; Indels 5; Gaps 4;
 QY 1061 ACACCGAAGCGCTGACGCTGCTCAACGACGACCACTGGCGGAGACCAAGTCTTCCACCAAA 1120
 Db 26 ATACGAGGCGCTGCGAGCTCTCTTACCGACAGTGGCAAGACCAAGTCTTCCACCAAA 85
 QY 1121 GCTTGGGAGCACTATGCGCGAGGCGCTTGCAGCGCGCTGCACCGGCTGCTGGAAGCGC 1180
 Db 86 GCTTGGGAGCACTATGCGCGAGGCGCTTGCAGCGCGCTGCACCGGCTGCTGGAAGCGC 145
 QY 1181 AGAAGGCATGCTAGAGAGCTGAGGAGGAGGAGCGCGCGCGAGCGCTGACCGCATGAGAC 1240
 Db 146 AGAAGGCATGCTAGAGAGCTGAGGAGGAGGAGCGCGCGCGAGCGCTGACCGCATGAGAC 205
 QY 1241 AGAAGTCCAGGCGCTACACGACGACCTGCGGAGGCTCCAGAGGAGGAGGAGGAGGAGG 1300
 Db 206 AGAAGTCCAGGCGCTACACGACGACGACGACGACGACGACGACGACGACGACGACGAC 265
 QY 1301 AGGAGGCGCTGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1360
 Db 266 AGGAGGCGCTGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 325
 QY 1361 AGCGGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1420
 Db 326 AGCGGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 385
 QY 1421 AGTACAGAGGCGCGCGCGAGTACAGCATGCTGGAAGGCGCTTCCAGAGCATCAGACCGCA 1480
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 QY 1481 TGGCAGCGCGCGCTTAACCTTGAGACCGCGGACAGCGCGCTGATCTGTGCGAGC 1540
 Db 446 TGGCAGCTGCGCTGAGACCATGAGACCGCGGACAGCGCGCTGATCTGTGCGAGC 505
 QY 1541 ACTGACCACTTGTGCTTACGCGCACTTGCACCGACGACGACGACGACGACGACGACGAC 1600
 Db 506 ACTGACCACTTGTGCTTACGCGCACTTGCACCGACGACGACGACGACGACGACGACGAC 565
 QY 1601 GCTTGCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1660
 Db 566 GCTTGCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 625
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 QY 1721 GCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1780
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 Db 746 ACGGTAAACGATGACAGCGCTGACAGAGGCGCTGAGCTAGGCTAACGTCCTCGGACAGC 805

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 17:45:16 ; Search time 102 Seconds
(without alignments)
1201.716 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504
Sequence: 1 MACSLKDELCSICLSIYQD.....GQSHANGKNVQPLRIYVRI 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organella:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2504	100.0	475	4	Q9BVG3
2	2491	99.5	475	4	Q9NVG0
3	763.5	30.5	609	13	Q92021
4	748.5	29.9	610	13	Q91431
5	664.5	26.5	496	11	Q8K0F7
6	662.5	26.5	488	4	Q81Y79
7	599.5	23.9	500	11	Q8VH26
8	577	23.0	513	11	Q8C205
9	576	23.0	513	11	Q891K1
10	572	22.8	506	11	Q62157
11	553.5	22.1	483	11	Q8VDC5
12	550.5	22.0	485	4	Q96PF7
13	550.5	22.0	485	4	Q8WZ70
14	550.5	22.0	511	4	Q96J90
15	539	21.1	470	11	Q921V6
16	523.5	20.9	485	11	Q8K243

17	520	20.8	501	11	Q8VID4	Q8VID4 mus musculus
18	520	20.8	501	11	Q8BYV9	Q8BYV9 mus musculus
19	520	20.8	516	11	Q8C006	Q8C006 mus musculus
20	513	20.5	470	11	Q8BVP1	Q8BVP1 mus musculus
21	501	20.0	471	4	Q8NA35	Q8NA35 homo sapien
22	500	20.0	468	4	Q8N9V2	Q8N9V2 homo sapien
23	483	19.3	504	4	Q9UPQ4	Q9UPQ4 homo sapien
24	480.5	19.2	341	4	Q8IYX3	Q8IYX3 homo sapien
25	475.5	19.0	477	11	Q9WV59	Q9WV59 rattus norv
26	459	18.3	477	4	Q9Y577	Q9Y577 homo sapien
27	458.5	18.3	296	4	Q8WY17	Q8WY17 homo sapien
28	456	18.2	545	6	Q77666	Q77666 sus scrofa
29	448	17.9	279	4	Q8WY16	Q8WY16 homo sapien
30	446.5	17.8	488	11	Q8BGE7	Q8BGE7 mus musculus
31	439	17.5	461	6	Q9TSM0	Q9TSM0 sus scrofa
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33	430	17.2	545	11	Q99PN3	Q99PN3 mus musculus
34	429	17.1	465	4	Q810X9	Q810X9 homo sapien
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37	421	16.8	519	13	Q91884	Q91884 xenopus lae
38	418	16.7	475	4	Q96PL5	Q96PL5 homo sapien
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40	418	16.7	475	11	Q8NCW2	Q8NCW2 homo sapien
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ALIGNMENTS

RESULT 1

Q9BVG3 ID Q9BVG3 PRELIMINARY; PRT; 475 AA.
AC Q9BVG3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC001222; AAH01222.1; -
DR EMBL; BC012152; AAH12152.1; -
DR EMBL; BC007999; AAH07999.1; -
DR EMBL; BC011689; AAH11689.1; -
DR InterPro: IPR001870; B302.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR006574; PRT.
DR InterPro: IPR003877; SPR_receptor.
DR InterPro: IPR00315; ZnF_Box.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00589; PRT; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00119; ZF_BOX; 1.
DR PROSITE; PS00518; ZF_RING; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 475 AA; 54267 MW; DC15CA9B795DFB0 CRC64;

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Best Local Similarity 100.0%; Pred. No. 6.2e-163;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MACSLKDELICISICISITQDPVSLGCEHYFCRCITTEHWVROEAGADCEPCRTFAEP 60

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DT 01-OCT-2000 (TREMblurel. 15, Last sequence update)
DT 01-MAR-2003 (TREMblurel. 23, Last annotation update)
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Iisogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoaka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kanehori K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DB EMBL; AK001621; BAA91792.1; -
DB InterPro: IPR001870; B302.
DB InterPro: IPR003006; B302.
DB InterPro: IPR003006; I9_MHC.
DB InterPro: IPR006574; PRY.
DB InterPro: IPR008877; SPRY_receptor.
DB InterPro: IPR000315; Znf_Box.
DB InterPro: IPR001841; Znf_fing.
DB Pfam; PF00622; SPRY; 1.
DB Pfam; PF00643; Zf-B_Box; 1.
DB Pfam; PF00097; Zf-C3HC4; 1.
DB SMART; SM00589; PRY; 1.
DB SMART; SM00184; RING; 1.
DB PROSITE; PS00290; IG_MHC; 1.

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DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 475 AA; 54190 MW; 7C04489D3B5C0F6C CRC64;

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Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 61 ALAPSLKLANIYVERYSSEPLDAIINARRAAPCOAHDKVKLFCLTDRLALCFCEDEPALH 120

OY 121 EOHVYTGIDDAFDELQRELKQQLQALQDSEHREHEALQLLKROLAETKSSKSLRTTIGE 180
DB 121 EOHVYTGIDDAFDELQRELKQQLQALQDSEHREHEALQLLKROLAETKSSKSLRTTIGE 180

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DB 181 AFERLHRLREROKAMLEELADTARTLTDIEOKVORYSOOLRKVOEGAOILOERLAETD 240

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DB 241 RHTELAGVASLSERLKGIHETNLTIEDPPTSKYTGPLQYTIWKSLEFODIHVPALATLD 300

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DB 301 PGTAHORILISDDCTIYAYGMLHPQLODSKRRDVEYSVLGSAFSSGCVHYWEVVAEK 360

OY 361 TQWVYIGLAHEAASRKSGIQIOPSRGFCYIVHNDGNQISACTEPTRLNVRKLDKVGVEL 420
DB 361 TQWVYIGLAHEAASRKSGIQIOPSRGFCYIVHNDGNQISACTEPTRLNVRKLDKVGVEL 420

OY 421 DYDGLLIFYNADMSWLYTEREKEPGKLCYSFSPGOSHANGKNVQPLRINTVRI 475
DB 421 DYDGLLIFYNADMSWLYTEREKEPGKLCYSFSPGOSHANGKNVQPLRINTVRI 475

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AC O92021;
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DT 01-NOV-1996 (TREMblurel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblurel. 23, Last annotation update)
DE XNF7-ZINC finger nuclear phosphoprotein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RA Reddy B.A., Kloc M., Etkin L.D.;
RL Submitted (APR-1991) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DB EMBL; S64515; AAB20269.1; -
DB EMBL; M63705; AAB49995.1; -
DB InterPro: IPR001870; B302.
DB InterPro: IPR000953; Chromo.
DB InterPro: IPR006574; PRY.

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DR InterPro: IPR003877; SPRY_Receptor.
DR InterPro: IPR000315; Znf_Box.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; Zf-B_Box; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00298; CHROMO; 1.
DR SMART: SM00589; PRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS50119; ZF_BOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 609 AA; 68875 MW; 088C8312B45C78F8 CRC64;

Query Match	30.5%	Score 763.5	DB 13	Length 609
Best Local Similarly	35.4%	Pred. No. 6e-44		
Matches 167; Conservative	88	Mismatches 200	Indels 17	Gaps 9

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Db	198	VLANIARAKAAPTVPYPERKTRPLEKSEHDERLKLCKDDGTLSCVCRSLKASINF	257
OY	126	TGIDAPDELORELKDOLQODSERHEATEALQILROLAETKSTKSL--RTTIGENF	182
Db	258	LPIIDAVGVYEEELSAIYAPLEASIKV-TE-QLSESDSKIECHNKMMOYKEHITSEF	314
OY	183	ERLRLREROKAMLEELADTARLITPIEQKORYSOQLRKROGAQIILERLAEYTRH	242
Db	315	EKLKFLPEREREKLLBOLKEGENILITMENNVKMOESODAIKTTISLAKFRMDIOSI	374
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Db	494	GDKTAMVDGMASSSNRGKRTIKLNPKNGYMAIWLNGNAYAKALEBPSKSLSSHPRIIG	553
OY	418	VFLDIYDQGLLIFYNADMSWLTYTREKPGKLCSTSPGQOSHANGKNVQPLR	469
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DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Nuclear factor 7.
CN	XNF7-O.
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoes; Pipidae;
CC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RM	MEDLINE=96081373; PubMed=8541218;
RX	Gong S.G., Reddy B.A., Etkin L.D.;
RA	"Two forms of Xenopus nuclear factor 7 have overlapping spatial but
RT	

RT different temporal patterns of expression during development.”;
RL Mech. Dev. 52:305-318(1995).
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; S80988; AAB35876.1; -.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR000315; ZnF_Box.
DR InterPro; IPR001841; ZnF_Fing.
DR Pfam; PF00662; SPRY_1.
DR Pfam; PF00643; Zf-B_Box_1.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SM00502; BHC; 1.
DR SMART; SM00336; BROX; 1.
DR SMART; SM00288; CHROMO; 1.
DR SMART; SM00589; PRY_1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY_1.
DR PROSITE; PS50119; ZF_BOX_1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 610 AA; 69115 MW; D828f60060572EC1 CRC64;

Query Match	29.98	Score 748.5	DB 13	Length 610
Best Local Similarity	33.48	Pred. No. 6.4e-43		
Matches 159; Conservative	94	Mismatches 198	Indels 25	Gaps 8

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OY 7 DELCISICLSIYODPVSJGCEHCYCRGICTEHMYROAOGARODPECRRTFAEALAPSL 66
Db 142 BELCPICLVEFKPDMVACGHNFCRSCIDVW--BQSSAPBEKESITTDKRTYINR 198
OY 67 KIANTIVERSPPLDAIIMARRAARPOQAND-KVLCPLCTDRALCCFCEDEPALAEHOY 125
Db 199 VLIANTAKCAACTPVYTPVEKTRPLEKSESEHDERLKCXKDQGLGVCYICRDSJLASHNF 258
OY 126 TGIDDADELORE-----LKDOLQLODBERHTEALOLKQLAETSSYKSLRTTI 178
Db 259 LPILDAIGVYNEELSAIYAPLEASLKTQEOLSGOSQKITEBHNNVNSOYKEHNTS----- 313
OY 179 GEAFERLRLREROKAMLEELDEADTARTLTDIEQKVOYRSQOLRKOVEGNOILORLAE 238
Db 314 --EERELKHFLAKEBEKRLBOLKQGNLITLEMENNYKMQENDALKRTISLAKEMEE 371
OY 239 TDRRTFLAGVASL----SERLKGIHETN-LTYEDFPYTKYTGLOQYTIWKSLEFODIHVY 293
Db 372 TDSISFLDITFDKCOEORAVISGTNLTLSKELCOGTEFGKIOYIMMELSLVTPPS 431
OY 294 PAALTLDPGTAHORLILSDCCTIYAQNLHQPRLDOSPBRDVEVSIVLSGAEFGVHW 353
Db 432 LTPHLIDPNASHPHLHSDGLTVRYGE-NKLSLDPNPKRSQCLITVSGSGFSGRHW 490
OY 354 EVVYAACEKOWYIGLAHEASRKSGIOLOPSRGFCYIWHGDOHQYSACTEPTRLYNDKL 413
Db 491 EVERGDKTAMVDYGMASESNNKGRKITLKNPKNGYAIMLRGNRRKALKESPKALSLSHP 550
OY 414 DKVGEVLDYDOGLLFTYADMSULYTFREKFPCKLSYSPSGOSHANGKRVOPLR 469
Db 551 KRIGVYVDEGGQISFYNADNMTLTYFSATFKTLYPVSIP-FLHDSGKNVALDR 605

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RESULT 5		
08K0F7		
ID	08K0F7	PRELIMINARY; PRT; 496 AA.
AC	08K0F7;	
DT	01-OCT-2002	(TREMBLrel. 22, Created)
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)
DE	Similar to tripartite motif protein 39.	
GN	TRIM39.	
OS	Mus musculus (Mouse).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Breast tumor;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; BC031540; AAH31540.1; -.
 DR MGD; MGI:1890659; Trm39.
 DR InterPro; IPR001870; B302.
 DR InterPro; IPR006574; PRY.
 DR InterPro; IPR003877; SPRY_Receptor.
 DR InterPro; IPR00315; Znf_Box.
 DR InterPro; IPR001841; Znf_Ring.
 DR Pfam; PF00622; SPRY; 1.
 DR Pfam; PF00643; zf-B_box; 1.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00336; BBOX; 1.
 DR SMART; SM00389; PRY; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS01019; zf_BOX; 1.
 DR PROSITE; PS00518; zf_RING_1; 1.
 DR PROSITE; PS00089; zf_RING_2; 1.
 DR Metal-Binding; Zinc; Zinc_Finger.
 KW SEQUENCE 496 AA; 57257 MW; 937B2558186C3D17 CRC64;
 SQ

Query Match 26.5%; Score 664.5; DB 11; Length 496;
 Best Local Similarity 33.7%; Pred. No. 2,6e-37;

Matches 168; Conservative 81; Mismatches 188; Indels 61; Gaps 12;

QY 4 SLKDELICSLISIVQDPVSLGCEHYFCRCITTEHWVQEOAGARD--CPECRRTFAAPA 61
 DB 22 NLQVANSVCLEIYKEVYIECGHNFCKACITRMWEDLE----RDFCPCVKRISRRS 77
 QY 62 LAPSLKLANIYERYSFPLDALINARRAARPC-QAHNDVKLFCLTRALLCFECDEPALH 120
 DB 78 LRPNQLGSWE--IAKOLQAVKRIKRIKDESICSPQHHEPLSLFCYEDQAVCLICASHTH 135
 QY 121 EOHQVGTGIDDAFDELQRELKQLOALODSREHTEALDLKROLAETKSTKSLRTTIGE 180
 DB 136 RPHVYVPDMDATQEKKEKLOKCLEPBOKLOEITCKSKSEKRPBELRLVSRROQLK 195
 QY 181 APERHLRLREROKAMLELEADTARTLTIDQKQVRSOOLRKVQEGAOILQERLAETD 240
 DB 196 EFEEHLRLRDEEOQLLSRLLEE-----EQDI-----LQRLRENAHLGDRRD-- 239
 QY 241 RHTFLAGVASLSERLKGR-----IHETNLTIEDPTSKYTG-----P 277
 DB 240 -----LAHLAAVEGKCLQSGFEMLDKDVSTLEKCKVKTMEVTSVILEKNFSNP 292
 QY 278 LQY-TIMKSLFQDHPV-----PALTLDPGTAHORLILSDCTIYAVGNLHPQLDPSK 332
 DB 293 ROYFALKRIKLQALAPLMLPRPADVTIDPETAHPLVLSEDRSKVFETRLRLDPTPQ 352
 QY 333 RFDVEVSLGSEAFSSGVHYWEVVAEKTQVYIGLAHEASRKSIOIQPSRGFYCIYMH 392
 DB 353 RFTFYCVLATGEFTSGRHYWEVEGDKTHNAVGVCRDSVSRKGLTLPLEPGYVRVLM 412
 QY 393 DGNQYSACTEPWTRLNVRDKLDKGVFLDYDQGLIFYNADMSLTYTREREKPGKLSY 452
 DB 413 NGDYVAATTPPTPLIKKPKRVGIFLDYEGATLSFYNVTDNRSHIYTFDTTEKIMPL 472
 QY 453 FSPGSHANGKNVQPLRI 470
 DB 473 FYPG-IRAGKKNAPLTI 489

RESULT 6
 081Y79 PRELIMINARY: PRT: 488 AA.
 ID 081Y79

AC 081Y79;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to tripartite motif protein 39.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Testis;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034985; AAH34985.1; -.
 SQ SEQUENCE 488 AA; 56374 MW; 102AABE5C8786A3E CRC64;

Query Match 26.5%; Score 662.5; DB 4; Length 488;
 Best Local Similarity 33.2%; Pred. No. 3,5e-37;

Matches 165; Conservative 79; Mismatches 186; Indels 67; Gaps 12;

QY 4 SLKDELICSLISIVQDPVSLGCEHYFCRCITTEHWVQEOAGARD--CPECRRTFAAPA 61
 DB 22 NLQVANSVCLEIYKEVYIECGHNFCKACITRMWEDLE----RDFCPCVKRISRRS 77
 QY 62 LAPSLKLANIYERYSFPLDALINARRAARPC-QAHNDVKLFCLTRALLCFECDEPALH 120
 DB 78 LRPNQLGSWE--IAKOLQAVKRIKRIKDESICSPQHHEPLSLFCYEDQAVCLICASHTH 135
 QY 121 EOHQVGTGIDDAFDELQRELKQLOALODSREHTEALDLKROLAETKSTKSLRTTIGE 180
 DB 136 RAHTVPIPDMDATQEKKEKLOKCLEPBOKLOEITCKSKSEKRPBELRLVSRROQLR 195
 QY 181 APERHLRLREROKAMLELEADTARTLTIDQKQVRSOOLRKVQEGAOILQERLAETD 240
 DB 196 EFEEHLRLRDEEOQLLSRLLEE-----EQDI-----LQRLRENAHLGDRRD-- 239
 QY 241 RHTFLAGVASLSERLKGR-----IHETNLTIEDPTSKYTG-----P 277
 DB 240 -----LAHLAAVEGKCLQSGFEMLDKDVSTLEKCKVKTMEVTSVILEKNFSNP 292
 QY 278 LQY-TIMKSLFQDHPV-----PALTLDPGTAHORLILSDCTIYAVGNLHPQLDPSK 333
 DB 293 ROYFALKRIKLQALAPLMLPRPADVTIDPETAHPLVLSEDRSKVFETRLRLDPTPQ 345
 QY 334 RFDVEVSLGSEAFSSGVHYWEVVAEKTQVYIGLAHEASRKSIOIQPSRGFYCIYMH 393
 DB 346 RFTFYCVLATGEFTSGRHYWEVEGDKTHNAVGVCRDSVSRKGLTLPLEPGYVRVLM 405
 QY 394 DGNQYSACTEPWTRLNVRDKLDKGVFLDYDQGLIFYNADMSLTYTREREKPGKLSY 453
 DB 406 GDKVAATTPPTPLIKKPKRVGIFLDYEGATLSFYNVTDNRSHIYTFDTTEKIMPL 465
 QY 454 SPGSHANGKNVQPLRI 470
 DB 466 FYPG-IRAGKKNAPLTI 481

RESULT 7
 08VHZ6 PRELIMINARY: PRT: 500 AA.
 ID 08VHZ6
 AC 08VHZ6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Ring finger-B box-coiled coil transcription factor.
 DE RN36.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6J; PubMed-11576878;
RX MEDLINE-21463391; PubMed-11576878;
RA Shyu H., Hsu S., Hsieh-Li H., Li H.,
RT "A novel member of the RBCC family, Trif, expressed specifically in
RT the spermatids of mouse testis.";
RL Mech. Dev. 108:213-216(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC EMBL; AF34958; AAA1031.1; -.
DR MGD; MGI:1918178; Rnf36.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00622; SPRY_1.
DR Pfam; PF00097; ZF-C3HC4_1.
DR SMART; SM00589; PRY_1.
DR SMART; SM00184; RING_1.
DR SMART; SM00449; SPRY_1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 500 AA; 57234 MW; 757907426D8AAE27 CRC64;

Query Match	23.9%	Score 599.5	DB 11	Length 500
Best Local Similarity	31.1%	Pred. No. 7.3e-33		
Matches 152; Conservative	81	Mismatches 206	Indels 49	Gaps 11

[illegible]

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA THE FANTOM Consortium,
 RA the Riken Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT Nature 420:563-573(2002)."
 RL EMBL: AK088180; BAC40192.1; -
 DR EMBL: AK088180; BAC40192.1; -
 SQ SEQUENCE 513 AA; 58550 MW; 97C4F14A003F6434 CRC64;

Query Match	23.0%	Score 577	DB 11	Length 513
Best Local Similarity	28.7%	Pred. NO. 2.6e-31		
Matches 149; Conservative	87;	Mismatches 190;	Indels 94;	Gaps 14;

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0Y 5 KDELICSGICSIYDDPSLGEHNEFCRCJITEHHVROEAOGARCPCEPREFAPALAP 64
Db 10 LQOETTCVCYCQIYFEPHMLDGSNHICCAICLARCMAEFTVNS--CPQCEFFPPRHMR 67
0Y 65 SLKIANIVERYSSPFLDAILNARRAP-----COAH-DKYLECFLDRAALLCEFC 114
Db 68 NRHLNLTWQ-----LVKQLFRERPSGPGEGVCEKHNEPILKICEDQDMPICVVC 118
0Y 115 DEPALHEHOYTGIDDAFDELQOREKDDQLAQDSERBETEROJLTKQ-----LAE 166
Db 119 DRSREHGHSAVPLEEAVEGFEQOJONRI-----DLRRVKOLKRRRAQGEQARAE 170
0Y 167 TKSSRKSRTTIGENAFERLHLRLEROKAMLEELADTARTLTDIEOKVORS----- 219
Db 171 LLSLTQMEREREKIVMEFEQOLYHSLKHEHYRLTLARLELDLAIYNSINGAITQSCNISHLS 230
0Y 220 -----QQLAKVQEGAOIIOERLAEIDR-----HTFLAGVASLSR 254
Db 231 GLIAOLEEQQOQPTLELLQDIDIGDYSRAERINIPERWITPPDLQEKIHIFPAOKCLPLETS 290
0Y 255 LKGIHETNLTIEDPPTSKRYTGPLQYTTWKSJLFODIHV--PAALTLDPTGAHORLILS 311
Db 291 LK-----QFTEKMQSDMEK--IQELREAOQLYSVDYTLDDPTAYPSLILS 332
0Y 312 DDCTIVAGNLHPQLDPSPKRFDVENVSYLSGEAASSGVHYAEVYVAETQWVIGLAIHA 371
Db 333 DNLROVRSTYLO-QOLPDNPERKFNLPCLVLSGPCMAGHNYEVEVGDAKARTIGVCES 391
0Y 372 ASRKSSIOIOPSRGQYCIYMHGNOYSACTEBWTRILNVADKLDKGVFLEIDQGLLIEFN 431
Db 392 VCRKGVSAPONGFWAVASLWYKREYMLTISPMTLALPRTPLQVRIGFILDYDAGEVSFYN 451
0Y 432 ADDMSWLYTF-REKFPGLKCSYFSQGSIAKNKNOPLRI 470
Db 452 VTERCHTETFSHATFCGVPVRPFS--LSTSYGSSAAPLII 489

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OC Mus musculus (Muscaea); Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090; [1]
RN
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DDJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: BC003219: AA03219.1: -
 DR MGD: MGI:97904: TrlM27.
 DR InterPro: IPR001870: B302.
 DR InterPro: IPR006574: PRY.
 DR InterPro: IPR003877: SPRY_receptor.
 DR InterPro: IPR000315: Znf_Box.
 DR InterPro: IPR01841: Znf_ring.
 DR Pfam: PF00622: SPRY, 1.
 DR Pfam: PF00643: Zf-B-box, 1.
 DR Pfam: PF00097: Zf-CHC4, 1.
 DR PRINTS: PR01406: BBOXZNFINGER.
 DR SMART: SM00336: BBOX, 1.
 DR SMART: SM00589: PRY, 1.
 DR SMART: SM00184: RING, 1.
 DR SMART: SM00449: SPRY, 1.
 DR PROSITE: PS50119: ZF_BOX, 1.
 DR PROSITE: PS00518: ZF_RING_1, 1.
 DR PROSITE: PS50089: ZF_RING_2, 1.
 DR Metal-binding: Zinc_finger.
 KW SEQUENCE 513 AA; 58512 MW; 9384B6678352A434 CRC64;

Query Match 23.0%; Score 576; DB 11; Length 513;
 Best Local Similarity 28.7%; Pred. No. 3, 1e-31;
 Matches 149; Conservative 87; Mismatches 190; Indels 94; Gaps 14;

QY 5 LKDELCSICLSITYDDPVSLGCEHYFCRCRTEHHVROAGARCPCECRFFAPALAP 64
 DB 10 LQOETTCPCVCLQYFEPFMDLDCGHNICACIARCGAETNVS--CPQCRTEFFPRHMP 67
 QY 65 SLKLANIVERYSSFLDAIILNARRARP-----COAH-DKYLFCTDTRALICFPC 114
 DB 68 NRHLNANVQ-----LVKQLRTERPSGPGCEMGVCEKHREPLKICEQDQMPICVVC 118
 QY 115 DEPALHEQOVTGIDAEDELQRELKQALQALQDSEHREHTEALQILKRO-----LAE 166
 DB 119 DRSREHGHSHVLPLEAVEGFEQIQNRL-----DHLRVKDKKRRRAQGOARAE 170
 QY 167 TKSSKSLRTTIGEAFFERHLRLRRQKAMLEELADRTARTLTDEQVQKRS----- 219
 DB 171 LLSLTOMEREKIVMEFQDLYHSLKEHYRLRLARLELDLAINYSINGALTQPSCNISLS 230
 QY 220 -----QOLRKVOEGAQIIQERLAETDR-----HTFLAGVASLSR 254
 DB 231 GLIALERKQOQPTRELLQDIDDTLSRAERIRIPRPWITPPLOEKIHIFNAOKCLEPES 290
 QY 255 LKGIHETNLYEDEPTSKYTGPLQYTIWKSLEFQDHPY---PAALTTDPGTAHQRLILS 311
 DB 291 LK-----QFTEKQSDMEK--IQELREQLYSVDYTLDPDTAPYSLILS 332
 QY 312 DDCTIVAGNLHROPLOSPKRFDEVSYLSEAFSSGVHYHVEVVAEKTQVIGLAHEA 371
 DB 333 DNLROVRSYILO-QDLPNPERFNLPCVLSPCFIARHNVWEVEVGDAKAKTIGVCES 391
 QY 372 ASRKSGSIQPSRGFYCIYMHGNOYSACTEPWTRLNVRDKIDKGVFLDYDOGLLIFYN 431
 DB 392 VCRKGGVSAPONGMVAWSLWYKREYALTSMTALPLRTPLQARIGIFLDIDAGEVSYN 451
 QY 432 ADDMSWLYTF-REKFPGLKSYFSPGQSHANGKNVQPLRI 470
 DB 452 VTERCHTFESHATFCGPVRPYFS--LSYSGKSAAPLII 489

RESULT 10
 Q62157
 ID 062157
 AC 062157;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Zinc finger protein (Freigment).
 GN TRIM27 OR RFP.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Takahashi M.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: X75343: CA453092.1: -
 DR MGD: MGI:97904: TrlM27.
 DR InterPro: IPR001870: B302.
 DR InterPro: IPR006574: PRY.
 DR InterPro: IPR003877: SPRY_receptor.
 DR InterPro: IPR000315: Znf_Box.
 DR InterPro: IPR01841: Znf_ring.
 DR Pfam: PF00622: SPRY, 1.
 DR Pfam: PF00643: Zf-B-box, 1.
 DR Pfam: PF00097: Zf-CHC4, 1.
 DR PRINTS: PR01406: BBOXZNFINGER.
 DR SMART: SM00336: BBOX, 1.
 DR SMART: SM00589: PRY, 1.
 DR SMART: SM00184: RING, 1.
 DR SMART: SM00449: SPRY, 1.
 DR PROSITE: PS50119: ZF_BOX, 1.
 DR PROSITE: PS00518: ZF_RING_1, 1.
 DR PROSITE: PS50089: ZF_RING_2, 1.
 DR DNA-binding: Metal-binding; Zinc_finger.
 FT NON_TER 1
 KW SEQUENCE 506 AA; 57882 MW; 2C6BEA626A1BED8 CRC64;

Query Match 22.8%; Score 572; DB 11; Length 506;
 Best Local Similarity 28.5%; Pred. No. 5, 6e-31;
 Matches 148; Conservative 88; Mismatches 190; Indels 94; Gaps 14;

QY 5 LKDELCSICLSITYDDPVSLGCEHYFCRCRTEHHVROAGARCPCECRFFAPALAP 64
 DB 3 LQOETTCPCVCLQYFEPFMDLDCGHNICACIARCGAETNVS--CPQCRTEFFPRHMP 60
 QY 65 SLKLANIVERYSSFLDAIILNARRARP-----COAH-DKYLFCTDTRALICFPC 114
 DB 61 NRHLNANVQ-----LVKQLRTERPSGPGCEMGVCEKHREPLKICEQDQMPICVVC 111
 QY 115 DEPALHEQOVTGIDAEDELQRELKQALQALQDSEHREHTEALQILKRO-----LAE 166
 DB 112 EPSREHGHSHVLPLEAVEGFEQIQNRL-----DHLRVKDKKRRRAQGOARAE 163
 QY 167 TKSSKSLRTTIGEAFFERHLRLRRQKAMLEELADRTARTLTDEQVQKRS----- 219
 DB 164 LLSLTOMEREKIVMEFQDLYHSLKEHYRLRLARLELDLAINYSINGALTQPSCNISLS 223
 QY 220 -----QOLRKVOEGAQIIQERLAETDR-----HTFLAGVASLSR 254
 DB 224 GLIALERKQOQPTRELLQDIDDTLSRAERIRIPRPWITPPLOEKIHIFNAOKCLEPES 283
 QY 255 LKGIHETNLYEDEPTSKYTGPLQYTIWKSLEFQDHPY---PAALTTDPGTAHQRLILS 311
 DB 284 LK-----QFTEKQSDMEK--IQELREQLYSVDYTLDPDTAPYSLILS 325
 QY 312 DDCTIVAGNLHROPLOSPKRFDEVSYLSEAFSSGVHYHVEVVAEKTQVIGLAHEA 371
 DB 326 DNLROVRSYILO-QDLPNPERFNLPCVLSPCFIARHNVWEVEVGDAKAKTIGVCES 384
 QY 372 ASRKSGSIQPSRGFYCIYMHGNOYSACTEPWTRLNVRDKIDKGVFLDYDOGLLIFYN 431
 DB 385 VCRKGGVSAPONGMVAWSLWYKREYALTSMTALPLRTPLQARIGIFLDIDAGEVSYN 444
 QY 432 ADDMSWLYTF-REKFPGLKSYFSPGQSHANGKNVQPLRI 470
 DB 445 VTERCHTFESHATFCGPVRPYFS--LSYSGKSAAPLII 482

RESULT 11


```

08VDX5
ID 08VDX5 PRELIMINARY; PRT; 483 AA.
AC 08VDX5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Similar to tripartite motif protein 11.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_Taxid=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL: BC020102; AAH20102.1; -
DR InterPro: IPR001870; B302.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR000315; ZnF_Box.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF006622; SPRY; 1.
DR Pfam: PF006643; zf-B_box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00589; PRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS50119; ZF_BOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 483 AA; 54313 MW; 51BDFCD514046FC CRC64;

Query Match 22.1%; Score 553.5; DB 11; Length 483;
Best Local Similarity 32.6%; Pred. No. 9.7e-30;
Matches 157; Conservative 77; Mismatches 194; Indels 53; Gaps 16;

QY 1 MACSLDELICSLISYODPVSLGCEHYFCRCRITENHWROBACGADCEGRFPAP 60
DB 6 LSTNLQDEATCALCIFYDPVMTDGHNCRCICRCWQPP--GVACPECELSAQR 63
QY 61 ALAPSLKLANIYERYSFPLDALILNRAARP-----COAH-DKVKLFCLTRALICF 112
DB 64 NLRPNPPLAKMAEM-----ARRLHPSPVPVQGYCAHREPLTTPCGDLSLCP 112
QY 113 FEDERPALHGHQVGTGIDAFDELQRELKQQLALQDSERHTEALQILKQLAET----K 168
DB 113 IC-ERSEHMTHRPQLQEAADDLKGRLKSLLEHL---RKQMEDAMLFQAQAEETCALWQ 167
QY 169 SSTKSLRTYIGAEFERLLRLREROKAMLEELADYARTLTIDIEOKVQRYSOOLRKVOEG 228
DB 168 KWESESROWNLGFEERLLRLAEBOOLQKLEEELEFVLRREGAARLGGQSTQIAL 227
QY 229 AQLIQR-----LAETDRHTFLAGVASLSERLKG--KIHEMLTYEDPFTSKYTP 277
DB 228 ISELERCOLPALGLQLCTECCLAREASIAKDICALCRVDVKLQ-----PPAVPME 283
QY 278 LQTTIK--SLPDIHVPALTLDPGTARQRLISDDCTIVAGNLHPPLQDSPPREF 335
DB 284 LR-TVCRVPLVETLRRFRGDTLDPGTANBELVLSDRRSVORGE-QORALPDNPERFD 341
QY 336 VEVSVLGSEAFSSGVHYMEVVAEKTQWVIGLAHEAASRKSGSIQIOPSRGFCYVMVDGN 395
DB 342 PGCVTLGQERITSGRIHYEVEVDQTSMALGVCKETANKREKELSGNFWLIVFL-GS 400
QY 396 QYSACEPTRLNVRDLKLVGVFLDYDQGLLIFTYNAADMSMLTYFEREK-FPGKLCYSF 454
DB 401 FYNSNBPASFPL--RDPKRVGIFLDYEAGHLSPYSATQDGLLFIPELTFSGTLRLFLS 458
QY 455 P 455

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DB 459 P 459
RESULT 12
096PF7
AC 096PF7 PRELIMINARY; PRT; 485 AA.
ID 096PF7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE SSA protein SS-56.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_Taxid=9606;
RP SEQUENCE FROM N.A.
RA MEDLINE-21445090; PubMed-11560955;
RA Billaut-Mulot O., Cocude C., Kolesnitchenko V., Truong M.J.,
RA Chan E.K., Hachulla E., de La Tribonniere X., Capron A., Bahr G.M.;
RT "SS-56, a novel cellular target of autoantibody responses in Sjogren
RT syndrome and systemic lupus erythematosus.";
RU J. Clin. Invest. 108:861-869(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL: AF360739; AAL1501.1; -
DR InterPro: IPR001870; B302.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR000315; ZnF_Box.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF006622; SPRY; 1.
DR Pfam: PF006643; zf-B_box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00589; PRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS50119; ZF_BOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 485 AA; 56319 MW; FCB9A61A5F7130A5 CRC64;

Query Match 22.0%; Score 550.5; DB 4; Length 485;
Best Local Similarity 29.3%; Pred. No. 1.6e-29;
Matches 150; Conservative 94; Mismatches 181; Indels 87; Gaps 17;

QY 4 SLDELICSLISYODPVSLGCEHYFCRCRITENW-VROBAG-ARDCECRRTFAEPA 61
DB 9 AIYEEVACPICMFLREPMSIDCGHSFCHSLSGLMEIPGESQWNGYTCPLCRAPVQPRN 68
QY 62 LAPSILKANIYERYSFPLDALILNRAARPQOAH-DKVLFLCLTDALICFCDEPALH 120
DB 69 LRPVQLANVVEVRLRLRHPGMGLK--GDLCERHGEKLMFKEDVLINCEASQSPER 126
QY 121 EOHQVGTGIDAFDELQRELQALQALQDSERHTEALQILKQLAET--KSTKSLRTTG 179
DB 127 EAHSVYMEVVAEYKWEHLBALEHLK--KQDEPMKLEVEGRKRTATWKLOVETRKQSI 185
QY 180 EAFERLLRLREROKAMLEELADYARTLTIDIEOKVQRYSOQLR---KVOGAQIQR 235
DB 186 WEFEKQRLLEKKOPH-RQLGAEVAAALASLOEAEFTQKLELNSESLIQSQVLMRM 244
QY 236 LAETDRHTFLAGVASLSERLKGKIHEMLTYEDPFTSKYTPLOTTWKSLPDI----- 290
DB 245 IAE-----LKERQRPVR-----W--MLADIQEVLN 268
QY 291 -----HVPAL-----TLDPGTARQRLISDDCTIVAG 320
DB 269 RSKMSLQGPPISELEKTDQCRVIGLREILKTYAADVRLDPDTRAYSILVISEDKRVHYG 328
QY 321 NLHPQLQDSPPKRDVEVSVLGSEAFSSGVHYMEVVAEKTQWVIGLAHEAASRKSGSIQI 380

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Db      329 DTN-QKLPDNPREFRYNIVLGSOCISSGRHWEVYDGRSEMGVGVCKQNDKREYVL 387
QY      381 OPSRGFYCIWMHDNQYSACTEPWTRLNVRDLKRVGLDYDOGLLIFYNADM-SMLY 439
Db      388 SPHYGFVYLRKKGNEYRAGTDEYPLISLPVPRRGVIGVDEADHSFYNTVDGSHIF 447
QY      440 TF-REKPGKLCYSFGQSHANGKNVOPLR 470
Db      448 TPRRYPPGRLPLPYSPCTS-IGTNNTAPLAI 478

RESULT 13
ID      08W270      PRELIMINARY;      PRT;      485 AA.
AC      08W270:
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Ro/SSA1 related protein FLJ10369.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Rhodes D.A., Allcock R.J.N., Trowdale J.;
RT      Cloning and characterization of FLJ10369, a novel Ro/SSA1-related
RT      gene on human chromosome 11p15.5.
RL      Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR      EMBL: AF439153; AAL31641.1; -.
DR      InterPro: IPR001870; B302.
DR      InterPro: IPR006574; PRY.
DR      InterPro: IPR003877; SPRY_receptor.
DR      InterPro: IPR000315; ZnF_Box.
DR      InterPro: IPR001841; ZnF_ring.
DR      Pfam: PF00622; SPRY.1.
DR      Pfam: PF00643; zf-B_box.1.
DR      Pfam: PF00097; zf-C3HC4.1.
DR      SMART: SM00336; BBOX.1.
DR      SMART: SM00589; PRY.1.
DR      SMART: SM00184; RING.1.
DR      SMART: SM00449; SPRY.1.
DR      PROSITE: PS00119; ZF_BOX.1.
DR      PROSITE: PS00518; ZF_RING_1.1.
DR      PROSITE: PS50089; ZF_RING_2.1.
KW      Metal-binding; zinc; zinc-finger.
SQ      SEQUENCE 485 AA; 56245 MW; 5F1C05A16384E033 CRC64;

Query Match      22.0%; Score 550.5; DB 4; Length 485;
Best Local Similarity 29.3%; Pred. No. 1.6e-29;
Matches 150; Conservative 94; Mismatches 181; Indels 87; Gaps 17;

QY      4 SIKDELICSLSTYODPVSLGCEHYFCRCITHEW-VRQAG-ARDCPCRRTFAPA 61
Db      9 AIVERVACPICMTFLREPMSIDCGSHSCISGLMEIPGSSQNGYCPICRAVQPRN 68
QY      62 LAPSLKLANIVERYSSPFLDAITLNARRAARPCQAH-DVKFICLUDRALLCFCDEPALH 120
Db      69 LRPMMQLANVYEVKRLRLHPGMGLK--GDLCEHGEKLMKFCREDVILMEACQSPEN 126
QY      121 ECHOVGTGIDAFDELQRLKQLOALQDSERHTEALQLKRLQALERT-KSSTKSLRTTIG 179
Db      127 EAHSPVEDVAMEKWEKHEALHEHLK-KEQEEAMKLEVGRRKRTATKIVETRKOSIV 185
QY      180 EAFRLRLRLEROKAMLEELADTARTLTIDIEQVQVYSOQLR-----KYDEGAQIIQER 235
Db      186 WEFEKYQRLLEKKQPPH-ROIGAEEVAAALASLQREAAETMOKLEINHSELIIQSOQVLMRM 244
QY      236 LAETDRHTFLAGVSLSERLKGKIHETNLTVEDEPTSKYTGPLQYTIKKSIFODI----- 290
Db      245 IAE-----LKERQRPVR-----W-MLODIQEVLN 268

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QY      291 -----HPVPAAL-----TLDPGTARQLITLSDCTIYAVG 320
Db      269 RSKMSIAQPEPISLELKTDCRVLAGRLKTYAGGVRLDPPTAASRLIVSDRRRVHG 328
QY      321 NHHQPLDQSPKRFDEVSVLSSEAFSSGVHWYEVVAEKTOVIGLAHAAASRRGSIOI 380
Db      329 DTN-QKLPDNPREFRYNIVLGSOCISSGRHWEVYDGRSEMGVGVCKQNDKREYVL 387
QY      381 OPSRGFYCIWMHDNQYSACTEPWTRLNVRDLKRVGLDYDOGLLIFYNADM-SMLY 439
Db      388 SPHYGFVYLRKKGNEYRAGTDEYPLISLPVPRRGVIGVDEADHSFYNTVDGSHIF 447
QY      440 TF-REKPGKLCYSFGQSHANGKNVOPLR 470
Db      448 TPRRYPPGRLPLPYSPCTS-IGTNNTAPLAI 478

RESULT 14
ID      09GJ90      PRELIMINARY;      PRT;      511 AA.
AC      09GJ90:
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Glycogenin-interacting protein 1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Skurat A.V., Dietrich A.D., Zhai L., Roach P.J.;
RT      Identification of human skeletal muscle proteins which interact with
RT      glycogenin.
RL      Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR      EMBL: AF396651; AAK85377.1; -.
DR      InterPro: IPR001870; B302.
DR      InterPro: IPR006574; PRY.
DR      InterPro: IPR003877; SPRY_receptor.
DR      InterPro: IPR000315; ZnF_Box.
DR      InterPro: IPR001841; ZnF_ring.
DR      Pfam: PF00622; SPRY.1.
DR      Pfam: PF00643; zf-B_box.1.
DR      Pfam: PF00097; zf-C3HC4.1.
DR      PRINTS: PR01406; BBOXZNFINGER.
DR      SMART: SM00336; BBOX.1.
DR      SMART: SM00589; PRY.1.
DR      SMART: SM00184; RING.1.
DR      SMART: SM00449; SPRY.1.
DR      PROSITE: PS00119; ZF_BOX.1.
DR      PROSITE: PS00518; ZF_RING_1.1.
DR      PROSITE: PS50089; ZF_RING_2.1.
KW      Metal-binding; zinc; zinc-finger.
SQ      SEQUENCE 511 AA; 56630 MW; 05C37C837A462597 CRC64;

Query Match      22.0%; Score 550.5; DB 4; Length 511;
Best Local Similarity 32.3%; Pred. No. 1.7e-29;
Matches 162; Conservative 65; Mismatches 207; Indels 67; Gaps 16;

QY      1 MASIKDELICSLSTYODPVSLGCEHYFCRCITHEWVQEA--QGAR-----DC 50
Db      19 LAELQEGATGSLCELEFREPVSVECGHSPCRACIGRWEPGAGSGVAAIRAPPPPLPC 78
QY      51 PECRRTAEPRLADSLKLANIVERYSSPFLDA-----TLNARRAARPCQAH-DVK 100
Db      79 PQCREPARPSQLRBNROLAAVATLIRPSLPAAAGEHGSOAAARAAARACGGHGPBK 138
QY      101 LFCULDRALLCFQDDEPALHGOHOVGTGIDDAFDELQRLKQLOA-----LQDSE-----RE 152
Db      139 LYCODDGRATCVCDRAHREHRAVLPLDEAVVOAKELLESRLVYLKKELEDCEVFST 198

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QY 153 HFEALQLLRQLAETSSSTKSLTTTGEAFERHLRLREROKAM---LEELADTAR--- 206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 199 KRESKELLKQMAEQRK-----VGAEFOALRAFLEVEQEGRLRLLELSREVAOKON 250
QY 207 -TTTDEKVRORSQOLRKVOEGAO-----ILOERLAETDRHTEFLAG--VASISELKGK 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 251 ENLAIQGVETITQSLSSQIOETROKPPDLTLOEFKSTLSRCSNVGPKPTVTSSEKKN 310
QY 259 IHTNLTYEDFPTSKYTPLOYYTWKSLPDH-----PYPALTTDPGTAHORLLISDD 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 311 VNVVSL-----KFEVLKGM-----KKFEDLNGELEKEKEKVELTIDPTANRLLISD 360
QY 314 CTIVAGNLHPOPLODSPKRFDEVSVLGSFAFSGVHWVVAEKTQWVIGLAHEAAS 373
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 LKGVRLGE-RAODLPHPHPCRFDTNTRVLASCGFSGRHHEVEVSGSKDGAFARESVR 419
QY 374 RKGSIQIOPSRGFCYVMHDGNOYSACTEPWTRFLNRDLDKYGVFLDIDOGLLITYMD 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 KRGLTFTPEBEGWALQL-NGGOYMAVTSPERSPLSCGHLRVALLDLEVGAVSYAVE 478
QY 434 DMSWLTFFREKFKGLCSYFS 454
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 479 DMRHLTYFRVNGERVFPLFS 499

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RESULT 15

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Q921V6 PRELIMINARY; PRT; 470 AA.
ID 0921V6
AC 0921V6:
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Sjogren syndrome antigen A1.
GN TRIM21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC010580; AA010580.1; -.
DR MGD; MGI:106657; Trim21.
DR InterPro: IPR001870; B302.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR000315; ZnF_Box.
DR pfam; PF00643; SPRY; 1.
DR pfam; PF00643; zf-B_box; 1.
DR pfam; PF00097; zf-C3HC4; 1.
DR PRINTS; PRO1406; BBOXZNFINGER.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PSS0119; ZF_BOX; 1.
DR PROSITE; PSS00518; ZF_RING_1; 1.
DR PROSITE; PSS0089; ZF_RING_2; 1.
KW Metal-binding; zinc; zinc-finger.
SQ SEQUENCE 470 AA; 54147 MW; DD91EEF5E398220C CRC64;

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Query Match 21.1%; Score 529; DB 11; Length 470;

Best Local Similarity 29.7%; Pred. No. 4.4e-28; Matches 146; Conservative 87; Mismatches 189; Indels 70; Gaps 18;

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QY 7 DELLSICLSIYDAPSLCEHYFCRCRTEHHVROEAQAGDPCRCRTFAEPALAPSL 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 16 EETVGSICIDPMWEPISIEGHCFCCKEIFE-----VGKNGSSCPECRQGFLLRNLPNR 71

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QY 67 KIANIYERSSFFLDAILNARRARP--COAH-DKYKLFCTDRALICFECDEPALHEOH 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 HIANVVENLKQI-----AQNTKSTOETHCRKHGEKLIHFCFEEGQALCWCAQSGKHRIH 127
QY 124 QVTVGIDAPDELRELKDQALODSREHTEALQ-LKRLQLAETSSSTSLTTTGEAF 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 TRVPIEAAKVYOEKTHVALEKLRK-KELAEKMEWDLTWQRDWMRNIDTORSRIHAEP 186
QY 183 ERLRLRLREROKAMLELEADTARTLTIDIEQKQVRSQOLRKVOEGAOILOERLAETDRH 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 ALQNSLLAQEENQALRLKEDQREYLRLLQKRE-----AELAEKNQALQELISLER- 238
QY 243 TFLAGVASLSERLKG---IHTNLTYE-----DEPTSKYTP-----LQY 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 -----RIRGSELELLQEVRLITLERSGSWNLDTLIDAPDLTSTCPVGRRKMLR 287
QY 281 TIKKSLFODIHPYPALTTDPGTAHORLLISDCTIYANGNLHPOPLODSPKRFDEVSV 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 TCW-----VH-----ITLDRNTANSWLLISKDRORVMDTH-QNVSDMKERFSNYPWV 335
QY 341 LGSEAFSGVHWVVAEKTQWVIGLAHEAASRKGSIQIOPSRGFCYVMHDGNOYSAC 400
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 LGAQRFSSGKMVYEDVYQKEMADLGYCRDSVQRKQFSLSPENGFTIWMQ-DSYEAG 394
QY 401 TEPWTRLNVRDLKRYGVFLDIDOGLLITYN-ADMSWLTFFRE-KFKGLCSYFSRQGS 458
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 395 TSPQTLHLIQVPPQIGIFVDYDAGVVSFYNIIDHGLIYTFSECVFAGLRPFNVGFN 454
QY 459 HANGKNVQPLRI 470
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 455 YSGG-NAAPLKL 465

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Search completed: October 7, 2003, 17:50:35
Job time : 105 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 17:50:42 ; Search time 67 Seconds

(without alignments)
1121.659 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504
Sequence: 1 MACSLKDELICSLCISTYOD.....GOSHANGKVQPLINTVRI 475

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications, AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2504	100.0	475	10	US-09-927-091-1
2	1312	52.4	304	10	US-09-927-091-2
3	613	24.5	500	10	US-09-731-872-466
4	613	24.5	500	12	US-09-876-997-466
5	583	23.3	580	9	US-09-925-301-943
6	492	19.6	465	12	US-10-024-298A-97
7	492	19.6	465	12	US-10-042-211A-97
8	489	19.5	465	12	US-10-024-298A-99
9	489	19.5	465	12	US-10-042-211A-99
10	418	16.7	475	12	US-10-000-897-78
11	388.5	15.5	194	10	US-09-764-868-1031
12	364.5	14.6	413	12	US-10-319-763-198
13	343.5	13.7	183	9	US-09-864-761-36547
14	339	13.5	584	10	US-09-910-174A-16
15	339	13.5	584	10	US-09-955-866-12

16	339	13.5	584	10	US-09-896-738-18	Sequence 18, Appl
17	339	13.5	584	12	US-10-041-319-17	Sequence 17, Appl
18	329	13.1	513	10	US-09-910-174A-18	Sequence 18, Appl
19	328	13.1	262	11	US-09-986-480-172	Sequence 172, App
20	328	13.1	262	15	US-10-205-823-105	Sequence 105, App
21	316.5	12.6	527	10	US-09-910-174A-10	Sequence 10, Appl
22	316.5	12.6	527	12	US-10-041-319-16	Sequence 16, Appl
23	316.5	12.6	527	15	US-10-156-424A-10	Sequence 10, Appl
24	315.5	12.6	529	10	US-09-910-174A-13	Sequence 10, Appl
25	313.5	12.5	535	12	US-10-137-870-124	Sequence 124, App
26	313.5	12.5	535	12	US-10-140-018-124	Sequence 124, App
27	313.5	12.5	535	12	US-10-140-021-124	Sequence 124, App
28	313.5	12.5	535	12	US-10-140-274-124	Sequence 124, App
29	313.5	12.5	535	12	US-10-140-471-124	Sequence 124, App
30	313.5	12.5	535	12	US-10-140-807-124	Sequence 124, App
31	313.5	12.5	535	12	US-10-140-807-124	Sequence 124, App
32	313.5	12.5	535	12	US-10-140-924-124	Sequence 124, App
33	313.5	12.5	535	12	US-10-140-926-124	Sequence 124, App
34	313.5	12.5	535	12	US-10-141-698-124	Sequence 124, App
35	313.5	12.5	535	12	US-10-141-702-124	Sequence 124, App
36	313.5	12.5	535	12	US-10-141-704-124	Sequence 124, App
37	313.5	12.5	535	12	US-10-142-421-124	Sequence 124, App
38	313.5	12.5	535	12	US-10-142-432-124	Sequence 124, App
39	313.5	12.5	535	12	US-10-142-767-124	Sequence 124, App
40	313.5	12.5	535	12	US-10-143-033-124	Sequence 124, App
41	313.5	12.5	535	12	US-10-144-994-124	Sequence 124, App
42	313.5	12.5	535	12	US-10-145-628-124	Sequence 124, App
43	313.5	12.5	535	12	US-10-145-633-124	Sequence 124, App
44	313.5	12.5	535	12	US-10-145-633-124	Sequence 124, App
45	313.5	12.5	535	12	US-10-145-746-124	Sequence 124, App

ALIGNMENTS

RESULT 1
US-09-927-091-1
Sequence 1, Application US/09927091
Patent No. US20020119541A1
GENERAL INFORMATION:
APPLICANT: KILLARY, ANN
APPLICANT: LOTT, STEVE
APPLICANT: CHANDLER, DAMN
TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
FILE REFERENCE: UTSC:651US
CURRENT APPLICATION NUMBER: US/09/927,091
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/227,560
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/225,033
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 475
TYPE: PRT
ORGANISM: Human
US-09-927-091-1

Query Match 100.0%; Score 2504; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.3e-202;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACSLKDELICSLCISTYODPVSLGCEHYCRRCITTHWVROEGARDCPECRRTFAEP 60
DB 1 MACSLKDELICSLCISTYODPVSLGCEHYCRRCITTHWVROEGARDCPECRRTFAEP 60
QY ALAPSLKIANIVERSSEFPDAILNARRARPCOAHDKVLFCTIDRALCFCDPEPALH 120
DB 61 ALAPSLKIANIVERSSEFPDAILNARRARPCOAHDKVLFCTIDRALCFCDPEPALH 120
QY 121 EGHQVGTIDDAFDELRELKQLOALQADSSREHTEALQLKROLAETKSSSTKSLRTTIGE 180
DB 61 EGHQVGTIDDAFDELRELKQLOALQADSSREHTEALQLKROLAETKSSSTKSLRTTIGE 180

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Db 121 EQHVTGIDDAFDELQRELKQDLOALODSERHEHTALQLLKRQLAETKSSKSLTATTGE 180
Qy 181 AFEHLRLRLRRQRKAMLEELBADTARLTLDIEQKQVRSQOLRKVQEGAOILQERLATD 240
Db 181 AFEHLRLRLRRQRKAMLEELBADTARLTLDIEQKQVRSQOLRKVQEGAOILQERLATD 240
Qy 241 RHTELAGVASLSEELKGIHETNLTIEDFPSTKTTGPRLOITKMSLFODIHVPALATLD 300
Db 241 RHTELAGVASLSEELKGIHETNLTIEDFPSTKTTGPRLOITKMSLFODIHVPALATLD 300
Qy 301 PGTAHQRLILSDDCITIAVAGNLHPQLDSDPKRFDVEVSIVGSEAFSSGVHWEVVAEK 360
Db 301 PGTAHQRLILSDDCITIAVAGNLHPQLDSDPKRFDVEVSIVGSEAFSSGVHWEVVAEK 360
Qy 361 TQWVIGLAHEAASRKSGSIQIDPSRGFYCIYMHNDGNOYSACTEPMTRLNVKDLKVGVEL 420
Db 361 TQWVIGLAHEAASRKSGSIQIDPSRGFYCIYMHNDGNOYSACTEPMTRLNVKDLKVGVEL 420
Qy 421 DYDGLLIFYNADMSWLTFRKFPKGLCSYFSPGSHANGKNOPLRINTVRI 475
Db 421 DYDGLLIFYNADMSWLTFRKFPKGLCSYFSPGSHANGKNOPLRINTVRI 475
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RESULT 2

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US-09-927-091-2
; Sequence 2, Application US/09927091
; Patent No. US20020119341A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOFT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: US/92/091
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 304
; TYPE: PRN
; ORGANISM: Human
US-09-927-091-2
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Query Match 52.4%; Score 1312; DB 10; Length 304;
Best Local Similarity 91.8%; Pred. NO. 2.8e-102;
Matches 257; Conservative 2; Mismatches 5; Indels 16; Gaps 1;
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Qy 1 MACSLKDELICISLISYQDPVSLGCEHYFCRCITTEHVMVROEAGARDCEPCRTFAEP 60
Db 1 MACSLKDELICISLISYQDPVSLGCEHYFCRCITTEHVMVROEAGARDCEPCRTFAEP 60
Qy 61 ALASLKLANTYVERYSFPLDAIINARRAAPCOAHDKVKLFCLTDRLALCFECDEPALH 120
Db 61 ALASLKLANTYVERYSFPLDAIINARRAAPCOAHDKVKLFCLTDRLALCFECDEPALH 120
Qy 121 EOHQVTVGIDDAFDELQRELKQDLOALODSERHEHTALQLLKRQLAETKSSKSLTATTGE 180
Db 121 EOHQVTVGIDDAFDELQRELKQDLOALODSERHEHTALQLLKRQLAETKSSKSLTATTGE 180
Qy 181 AFEHLRLRLRRQRKAMLEELBADTARLTLDIEQKQVRSQOLRKVQEGAOILQERLATD 240
Db 181 AFEHLRLRLRRQRKAMLEELBADTARLTLDIEQKQVRSQOLRKVQEGAOILQERLATD 240
Qy 241 RHTELAGVASLSEELKGIHETNLTIEDFPSTKTTGPRLOITKMSLFODIHVPALATLD 300
Db 241 RHTELAGVASLSEELKGIHETNLTIEDFPSTKTTGPRLOITKMSLFODIHVPALATLD 300
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RESULT 3

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US-09-731-872-466
; Sequence 466, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78. US3. REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 466
; LENGTH: 500
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-731-872-466
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```
Query Match 24.5%; Score 613; DB 10; Length 500;
Best Local Similarity 31.6%; Pred. NO. 4e-43;
Matches 148; Conservative 83; Mismatches 222; Indels 16; Gaps 8;
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Qy 8 ELICISLISYQDPVSLGCEHYFCRCITTEHVMVROEAGARDCEPCRTFAEPALAPSLK 67
Db 38 ELICPLCDMFRDPLMLSCGHNFCACIODWRLQAKE--TFCECKMLCOYNNCTPNPV 95
Qy 68 LANIYERYSFPLDAIINARRAAPCOAH-DVKLFCLTDRLALCFECDEPALH--EQHQ 124
Db 96 LDKLVEKIKRLP-----LKGHPCCPEHGENMLKFSKPDGKLCFCQCKDARLVSGOSKE 149
Qy 125 VTGIDDAFDELQRELKQDLOALODSERHEHTALQLLKRQLAETKSSKSLTATTGEAEP 184
Db 150 FLQISDAVHFMEEELAIQGOLETTKLQTLRNQKKAIAHNEKNLHTDOHVSMEFLK 209
Qy 185 LHLRLRRQRKAMLEELBADTARLTLDIEQKQVRSQOLRKVQEGAOILQERLATDRTPT 244
Db 210 LHPFLSKEXKIDLTREBEGKALNEMELNLSQLOEGCLLAKMLVYSIQATBOONSDF 269
Qy 245 LAGVASLSEELKGIHETNLTIEDFPSTKTTGPRLOITKMSLFODIHVPALATLDP 301
Db 270 LKDIITTLHSLDEQGMKVLATRELISRKLNIGQYKPIQYVWVREMQDTLCPLSLTLDP 329
Qy 302 GTAHQRLILSDDCITIAVAGNLHPQLDSDPKRFDVEVSIVGSEAFSSGVHWEVVAEKT 361
Db 330 KTAHNLVLSKSGTQSVWHGDI-KKIMPDPERFSSVAVLDSRGFTSGKMWEEVVAEKT 388
Qy 362 QWVIGLAHEAASRKSGSIQIDPSRGFYCIYMHNDGNOYSACTEPMTRLNVKDLKVGVEL 421
Db 389 KMTGVVAVRESITIRKSGSCPLTEPGQFWMLRLANQDILKALDLPSPSLITLNNLDKVGITLD 448
Qy 422 YDGLLIFYNADMSWLTFRKFPKGLCSYFSPGSHANGKNOPLRINTVRI 470
Db 449 YEGQLSFYNAKTMHTHTYFNTFMEKLYPYFCPLNDGR-ENKEPLHI 496
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RESULT 4

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US-09-876-997-466
; Sequence 466, Application US/09876997
; Patent No. US20030152921A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78. US3. CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
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; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO: 466
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-997-466

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Query Match      24.5%; Score 613; DB 12; Length 500;
Best Local Similarity 31.6%; Pred. No. 4e-43;
Matches 148; Conservative 83; Mismatches 222; Indels 16; Gaps 8;

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QY 8 ELICSLICSLIYDDPVSLGCEHYFCRCRITENHWROGAQADCEPCRRTPAEPALPSLK 67
DB 38 ELHCPLCNDWFDPLMLSCGHNEFCACIDFWRLOAKE--TFCPECKMLCQYNNCTFNPV 95
QY 68 LANIYERYSFPLDAIILNARRAAPCOAH-DKVKLECLTDRALLCFCEDEPALH--EQHQ 124
DB 96 LDKIVKIKKPL-----LKGHPQCPHGENIKLFSKPDGKILICQCKDARLSVGOSKE 149
QY 125 VMGIDDAFDELQRELKQALQADSEREHTALQLKROLAETKSSTKSLRTTIGEAFAER 184
DB 150 FLQISPAVHFMEELAIQOGQLETTLEKQLTLENNQKALAAKEMKHLQHVSMELK 209
QY 185 LIRLLEROKAMLEELADPARTLIDIEQKQVRSQQLKRVQGAQIIDGERLAETDRHTF 244
DB 210 LHQFHSKSKEDITTEEREGKALNEMELNLSQLOQCLLAKMLVSIQAKTQOQNSFDP 269
QY 245 LAGVASLSERLKG--KIHET-NLTYEDFPSTKYTGFLQYTIWKSLEFODIHVPALTLDP 301
DB 270 LMDITLHLSLEGKMYLVARRELISRKLNIGQYKGIQYVWREMDTLCPSPLTLDP 329
QY 302 GRNHOQLISDCTIYAGNLHPQLQDSPKRPDEVSVLGSFAFSGVHYWEVVAEKT 361
DB 330 KTAHPMLVLSKQTSYVWHDII--KKIMDPDEREDSVAVLGSRGTSKMYWEVVAEKT 388
QY 362 QNVIGLAHEAASRKSIOIOPSRGFCYIWMHGNQVSACEPTRLNVRKIDKLVGYELD 421
DB 389 KATVGAVRESILIKGSCPLTEPGGFWLRLRNQTDIKALDLPFSFSLTLNNLDKVGITYLD 448
QY 422 YDQGLLIIFYNADMSWLYTFREKFPGLKCSYFSPGSHANGKVVOPLRI 470
DB 449 YEGQSLFTYNAKTMTHITFTFSNTFMKILYFPCPLNDGR-EKKEPLHI 496

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RESULT 5
; Sequence 943, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO: 943
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (52)

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-943

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Query Match      23.3%; Score 583; DB 9; Length 580;
Best Local Similarity 29.1%; Pred. No. 1.7e-40;
Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;

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DB 77 LQOETTCVPCLOLYFAEPMMLDGCNHCACIACIACACGTAAETNVS--CPQCHETPORHMR 134
QY 65 SLKLANIYERYSFPLDAIILNARRAAP-----COAH-DKVKLECLTDRALLCFCE 114
DB 135 NRIILANVTQ-----LVKQURTERPSPGGEMGVCENHREPLKICEDDMPICVC 185
QY 115 DEPALHQHGVTSIDAFDELQRELKQALQADSEREHTALQLKRO-----LAE 166
DB 186 DRSREHGHSHVLPLEAEVGEFKQIQNQL-----DHLKRVKDLKRRRAQEGQARAE 237
QY 167 TKSTSLRTTIGEAERLRLARE--RQKAMLEEL-----ADTA 205
DB 238 LLSLTQMEREKIWEEDQLYHSLSKEHEYLRLARLELDLAIVNSINGATQFSCNTSHLS 297
QY 206 RFLTDIEQKQVRSQQLKRVQGAQIIDGERLAETDR-----HTFLAGV 248
DB 298 SLIAQLEKQOQPTREL-----LQDIGDTLSAERIRIPEPITPPDQEKHITRQK 351
QY 249 ASLSERLKGKIHETNLTIEDFPSTKYTGFLQYTIWKSLEFODIHVP--PALTLDPGTAH 305
DB 352 LFLTESLK-----QTEKMQSDMER--IQELREAQULYSVDVTLDPDTAV 393
QY 306 QRLISDCTIYAGNLHPQLQDSPKRPDEVSVLGSFAFSGVHYWEVVAEKTQVYI 365
DB 394 PSILISDNLKQVRYSTLQ--QDLPDNERFLFPCLVSSPCFIFGRHYWEVVAEKTQVYI 452
QY 366 GLAHEAASRKSIOIOPSRGFCYIWMHGNQVSACEPTRLNVRKIDKLVGYELDQ 425
DB 453 GVEDDSVCRKGGVTSAPQNGFMAVSLMYGLEYALNLSPTALDLRLPQLQVNGIFLDYDAG 512
QY 426 LLIFYNADMSWLYTF--REKFPGLKCSYFSPGSHANGKVVOPLRI 470
DB 513 EVSFYVWTERCHTFESHATFCGPVPYRFS--LSYSGKSAADLI 556

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RESULT 6
US-10-024-298A-97
; Sequence 97, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-kB Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28

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; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 465
; TYPE: prt
; ORGANISM: Homo sapiens
;
US-10-024-298A-97

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Query Match	19.68;	Score 492;	DB 12;	Length 465;
Best Local Similarity	29.38;	Pred. No. 5.5e-33;		
Matches 137;	Conservative 80;	Mismatches 206;	Indels 44;	Gaps 11

[illegible]

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1 RESULT 7
2 US-10-042-211A-97
3 Sequence 97, Application US/10042211A
4 Publication NO. US20030170719A1
5 GENERAL INFORMATION:
6 APPLICANT: MATSUDA, Akio et al.
7 TITLE OF INVENTION: NFKB Activating Gene
8 FILE REFERENCE: 1254-0192P
9 CURRENT APPLICATION NUMBER: US/10/042,211A
10 CURRENT FILING DATE: 2002-01-11
11 PRIOR APPLICATION NUMBER: JP 2000-402288
12 PRIOR FILING DATE: 2000-12-28
13 PRIOR APPLICATION NUMBER: JP 2001-088912
14 PRIOR FILING DATE: 2001-03-26
15 PRIOR APPLICATION NUMBER: JP 2001-254018
16 PRIOR FILING DATE: 2001-08-24
17 PRIOR APPLICATION NUMBER: US 60/258,315
18 PRIOR FILING DATE: 2000-12-28
19 PRIOR APPLICATION NUMBER: US 60/278,640
20 PRIOR FILING DATE: 2001-03-26
21 PRIOR APPLICATION NUMBER: US 60/314,385
22 PRIOR FILING DATE: 2001-08-24
23 NUMBER OF SEQ ID NOS: 102
24 SOFTWARE: PatentIn Ver. 2.0
25 SEQ ID NO 97
26 LENGTH: 465
27 TYPE: PRT
28 ORGANISM: Homo sapiens

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US-10-042-211A-97

Query Match	19.6%;	Score 492;	DB 12;	length 465;
Best Local Similarity	29.3%;	Pred. NO. 5.5e-33;		
Matches 137;	Conservative 80;	Mismatches 206;	Indels 44;	Gaps 11;

[illegible]

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US-RESULT 8
US-10-024-298A-99
: Sequence 99, Application US/10024298A
: Publication No. US20030143540A1
: GENERAL INFORMATION:
: APPLICANT: ASahi KASEI KABUSHIKI KAISHA
: APPLICANT: AKIO MATSUDA
: APPLICANT: Goichi HONDA
: APPLICANT: Shuji MORIMATSU
: APPLICANT: Yukiko NAGAO
: TITLE OF INVENTION: NF-K B Activating Gene
: FILE REFERENCE: 1154-0191P
: CURRENT APPLICATION NUMBER: US/10/024,298A
: PRIORITY FILING DATE: 2003-04-08
: PRIOR APPLICATION NUMBER: 60/314,385
: PRIOR FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: 60/278,641
: PRIOR FILING DATE: 2001-03-26
: PRIOR APPLICATION NUMBER: 60/258,315
: PRIOR FILING DATE: 2000-12-28
: PRIOR APPLICATION NUMBER: JP254018/2001
: PRIOR FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: JP0086912/2001
: PRIOR FILING DATE: 2001-03-26
: PRIOR APPLICATION NUMBER: JP402288/2000
: PRIOR FILING DATE: 2000-12-28
: NUMBER OF SEQ ID NOS: 182
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 99
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-024-298A-99

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 17:38:16 ; Search time 85 Seconds

(without alignments)
887.001 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504
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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2491	99.5	475	23	AAU78657 Human tumour suppressor
3	1312	52.4	304	23	AAU78657 Human tumour suppressor
4	634	23.3	123	22	AAU78657 Human tumour suppressor
5	631	25.2	735	22	AAU78657 Human tumour suppressor
6	613	24.5	500	22	AAU78657 Human tumour suppressor
7	583	23.3	580	21	AAU78657 Human tumour suppressor
8	560	22.4	468	23	AAU78657 Human tumour suppressor
9	552.5	22.1	475	12	AAU78657 Human tumour suppressor

10	550.5	22.0	485	23	ABP64866 Human protein seq
11	550.5	22.0	485	23	AAU78657 Human tumour suppressor
12	550.5	22.0	485	23	AAU78657 Human tumour suppressor
13	520	20.8	516	22	AAU78657 Human tumour suppressor
14	505.5	20.2	488	22	AAU78657 Human tumour suppressor
15	499.5	19.9	467	23	ABP70085 Human protein seq
16	492	19.6	465	23	ABP70085 Human protein seq
17	489	19.5	465	19	AAU78657 Human tumour suppressor
18	489	19.5	465	19	AAU78657 Human tumour suppressor
19	487	19.4	465	23	ABP61473 Human protein seq
20	483	19.3	493	22	AAU78657 Human tumour suppressor
21	483	19.3	504	22	AAU78657 Human tumour suppressor
22	475.5	19.0	461	22	AAU78657 Human tumour suppressor
23	458	18.3	477	21	AAU78657 Human tumour suppressor
24	449	17.9	539	24	ABU03729 Human protein seq
25	449	17.9	539	24	ABU03729 Human protein seq
26	449	17.9	539	24	ABU03729 Human protein seq
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29	427.5	17.1	781	23	AAU78657 Human tumour suppressor
30	422.5	16.9	477	20	AAU78657 Human tumour suppressor
31	418	16.7	475	21	AAU78657 Human tumour suppressor
32	418	16.7	475	23	ABP50231 Human protein seq
33	414.5	16.6	488	22	ABP50231 Human protein seq
34	413.5	16.5	488	22	ABP50231 Human protein seq
35	413.5	16.5	488	22	ABP50231 Human protein seq
36	411	16.4	483	22	AAU78657 Human tumour suppressor
37	411	16.4	483	22	AAU78657 Human tumour suppressor
38	410.5	16.4	493	22	AAU78657 Human tumour suppressor
39	409	16.3	579	23	ABP50231 Human protein seq
40	393	15.7	488	21	AAU78657 Human tumour suppressor
41	388.5	15.5	194	22	AAU78657 Human tumour suppressor
42	383	15.3	518	22	AAU78657 Human tumour suppressor
43	381.5	15.2	435	22	AAU78657 Human tumour suppressor
44	376	15.0	483	21	AAU78657 Human tumour suppressor
45	364.5	14.6	413	20	AAU78657 Human tumour suppressor

ALIGNMENTS

RESULT 1	AAU78657	AAU78657 standard; Protein; 475 AA.
XX	XX	AAU78657;
XX	XX	18-JUN-2002 (first entry)
DE	XX	Human tumour suppressor CAR-1.
XX	XX	Human: tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW	XX	gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW	XX	colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW	XX	prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW	XX	head and neck cancer; oesophageal cancer; bone marrow cancer;
XX	XX	chromosome 1p31-1p36.
OS	XX	Homo sapiens.
PN	XX	WO200212285-A2.
PD	XX	14-FEB-2002.
PF	XX	09-AUG-2001; 2001WO-US25269.
PK	XX	10-AUG-2000; 2000US-225033P.
PR	XX	23-AUG-2000; 2000US-227560P.
PA	XX	(TEXA) UNIV TEXAS SYSTEM.
XX	XX	Killary A. Chandler D. Lott S;
PI	XX	

DR MPI: 2002-269088/31.
 XX N-PSDB; ABR12806.
 PT New tumour suppressor CAR-1 polypeptides and polynucleotides, useful for
 PT diagnosing cancer, for altering the phenotype of a tumour cell, for
 PT treating cancers or as a diagnostic or prognostic indicator of cancer
 PT -
 XX
 XX
 XX Claim 23; Page 131-132; 185pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a
 CC polypeptide being tumour suppressor, CAR-1. Also included are
 CC fragments of the polynucleotide from 15-5000 nucleotides; fragments of
 CC the protein from 10-50 amino acids; an expression cassette comprising the
 CC polynucleotide under the control of a promoter operable in eukaryotic
 CC cells; a method for suppressing growth of a cancer cell by contacting
 CC the cells with the expression cassette (i.e. gene therapy); a cell
 CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody; a hybridoma cell that produces the monoclonal
 CC antibody; a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject;
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1, or by
 CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC non-transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases
 CC of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer,
 CC for altering the phenotype of a tumour cell, for treating cancers (e.g.
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
 CC other tissues), and as a diagnostic or prognostic indicator of cancer.
 CC CAR-1 may also be used in screening compounds for activity in either
 CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking
 CC the effect of mutant CAR-1 molecule. The gene for CAR-1 is located
 CC on chromosome 1 (1p31-1p36). The present sequence represents human CAR-1.
 CC
 XX
 XX Sequence 475 AA;
 SQ
 Query Match 100.0%; Score 2504; DB 23; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.7e-208;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 PGTARQLILSDCTIVAYGNLHPQLDSPRRFDEVSVLGSEAFSSGVHWYVAEK 360
 DB 301 PGTARQLILSDCTIVAYGNLHPQLDSPRRFDEVSVLGSEAFSSGVHWYVAEK 360
 OY 361 TQWVIGLHMAASRRGSIQIQPSRGFCYVHWDGQYSACNCEPTRLVNRKLDKRGVFL 420
 DB 361 TQWVIGLHMAASRRGSIQIQPSRGFCYVHWDGQYSACNCEPTRLVNRKLDKRGVFL 420
 OY 421 DYDGLILFYNADSMWLYTFREKPGKICSYFSPGSHANGKNQPLRINTVRI 475
 DB 421 DYDGLILFYNADSMWLYTFREKPGKICSYFSPGSHANGKNQPLRINTVRI 475
 RESULT 2
 AAB93138
 ID AAB93138 standard; Protein; 475 AA.
 XX
 AC AAB93138;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:12037.
 XX
 KM Human; primer: detection; diagnosis; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegaki T, Mshikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR MPI: 2001-316749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 12037; 2537bp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

CC of the present invention.

CC of the present invention.

SQ Sequence 475 AA;

Query Match	99.5%	Score 2491;	DB 22;	Length 475;

Best Local Similarity 99.6%; Pred. No. 2.3e-207;

Matches 4 / 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MASCSLKDELKLSICISCTIYODPVLSCENHFCRCRCITENHWRODAQARCPPECRRTPAEP	60
Dp	1	MASCSLKDELKLSICISCTIYODPVLSCENHFCRCRCITENHWRODAQARCPPECRRTPAEP	60
QY	61	ALAPSLKLANIYERYSSEPLDAILNARRAARPCQAHDKVKLCPLCTDRALCFPCDDEPALH	120
Dp	61	ALAPSLKLANIYERYSSEPLDAILNARRAARPCQAHDKVKLCPLCTDRALCFPCDDEPALH	120
QY	121	EOHOUTGIDDAFDELOREKLOLOALQDSEBRENTEALQILKRLQATKSKTSKSLRPTIGE	180
Dp	121	EOHOUTGIDDAFDELOREKLOLOALQDSEBRENTEALQILKRLQATKSKTSKSLRPTIGE	180
QY	181	AFERLHRLRLREROKAMLELEADPTARTLTDIEQOKARYSQOLRKYVQEGAOILQERLAEPTD	240
Dp	181	AFERLHRLRLREROKAMLELEADPTARTLTDIEQOKARYSQOLRKYVQEGAOILQERLAEPTD	240
QY	241	RHTFLAGVASISERLKGKIHEHTNLTYEDEPSTSKYTGPIQYTTWKSLEFODIHVPYPAALVTTD	300
Dp	241	RHTFLAGVASISERLKGKIHEHTNLTYEDEPSTSKYTGPIQYTTWKSLEFODIHVPYPAALVTTD	300
QY	301	PGTAHORLILSDQCTIVAGNHLHPLODSPRPFDEVSVLGSSEARSSGVNHYEYVAAEK	360
Dp	301	PGTAHORLILSDQCTIVAGNHLHPLODSPRPFDEVSVLGSSEARSSGVNHYEYVAAEK	360
QY	361	TQWVYIGLAHEAASRRGSIQIOPSRGYYCTIYMDGNDQYSACTBEPWTRLNVADKLDKYGVEL	420
Dp	361	TQWVYIGLAHEAASRRGSIQIOPSRGYYCTIYMDGNDQYSACTBEPWTRLNVADKLDKYGVEL	420
QY	421	DYDQGLILFYNAADMSWLTFRREKPPGKLCSTFSPQOSIANGKNVOPRLINTVRI	475
Dp	421	DYDQGLILFYNAADMSWLTFRREKPPGKLCSTFSPQOSIANGKNVOPRLINTVRI	475

RESULT 3
AAU78658
ID AAU78658 standard; Protein; 304 AA

AC AAU78658;

DT 18-JUN-2002 (first entry)

Human tumour suppressor CAR-1 produced by alternative splicing

KW Human; tumour suppressor: CAR-1; cytoskeletal; cancer; tumour;
 KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer
 KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
 KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
 KW head and neck cancer; oesophageal cancer; bone marrow cancer;
 KW chromosome 1p31-1p36.

OS Homo sapiens.

PN W0200212285-A2.

PD 14-FEB-2002

09-AUG-2001; 2001WO-US25269.

PR 10-AUG-2000; 200005-225033P
PB 23-AUG-2000; 200005-2337560P

XX
XX
PA / TEXA) INTV TEXAS SYSTEM

XX

PI Killary A, Chandler D, Lott S,

WPI; 2002-269088/31

PT New tumour suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumour cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer
PT -

PS Claim 23; Page 133; 185pp; English.

The invention relates to an isolated polynucleotide encoding a polypeptide being tumour suppressor, CAR-1. Also included are fragments of the polynucleotide from 15-5000 nucleotides; fragments of the protein from 10-50 amino acids; an expression cassette comprising the polynucleotide under the control of a promoter operable in eukaryotic cells; a method for suppressing growth of a cancer cells by contacting the cells with the expression cassette (i.e. gene therapy); a cell comprising the expression cassette; an anti-CAR-1 monoclonal or polyclonal antibody; a hybridoma cell that produces the monoclonal antibody; a method of diagnosing a cancer by assessing the expression of CAR-1 tumour suppressor in the cells of a tissue sample from a subject; methods for altering the phenotype of a tumour cell, methods for treating a subject with cancer by administering the tumour suppressor CAR-1, or by administering a nucleic acid encoding the tumour suppressor CAR-1 and a promoter active in eukaryotic cells, where the promoter is operably linked to the region encoding the tumour suppressor, a non-human transgenic eukaryote lacking a functional CAR-1 gene, a non-human transgenic eukaryote that over-expresses CAR-1 as compared to a similar non-transgenic eukaryote; a method of screening a candidate substance for anti-tumour activity by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance and determining the effect of the candidate substance on the cell; contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance, determining the effect of the candidate substance on the cell; identifying a candidate inhibitor substance; and making a composition and an isolated and purified nucleic acid that hybridizes, under high stringency conditions, to a DNA segment comprising about 15-3826 bases of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for altering the phenotype of a tumour cell, for treating cancers (e.g. cancer of the brain, lung, liver, kidney, lymph node, pancreas, small intestine, blood cells, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or other tissues), and as a diagnostic or prognostic indicator of cancer. CAR-1 may also be used in screening compounds for activity in either stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the effect of mutant CAR-1 molecule. The gene for CAR-1 is located on chromosome 1 (1p31-1p36). The present sequence represents a variant human CAR-1 produced by alternative splicing of the CAR-1 cDNA.

SQ Sequence 304 AA;

Query Match	52.48;	Score 1312;	DB 23;	Length 304;
Query Match	52.48;	Score 1312;	DB 23;	Length 304;

Best Local Similarity 91.8%; Pred. No. 2.7e-105;

malcles 231; conservative 4; mismatches 5; indels 16; gaps 1;

QY	MACSLKDELCLCSICLSITODPVSIGENHFCRCITTEHMVNOAGNADCECRRTPAEP	60
Db	1 MACSLKDELCLCSICLSITODPVSIGENHFCRCITTEHMVNOAGNADCECRRTPAEP	60
QY	ALAPSLKLANIYERYSFPFLDAILNARRAAPQCAHDFVKLECTLDRALCLFCFCEPALH	120
Db	61 ALAPSLKLANIYERYSFPFLDAILNARRAAPQCAHDFVKLECTLDRALCLFCFCEPALH	120
QY	ECHQVYGVGIDDAFELORELKDOLQALQDSERHEHTALQLLKROLAETKSSKTSKRTTIGE	180
Db	61 ECHQVYGVGIDDAFELORELKDOLQALQDSERHEHTALQLLKROLAETKSSKTSKRTTIGE	180
QY	ECHQVYGVGIDDAFELORELKDOLQALQDSERHEHTALQLLKROLAETKSSKTSKRTTIGE	180
Db	121 ECHQVYGVGIDDAFELORELKDOLQALQDSERHEHTALQLLKROLAETKSSKTSKRTTIGE	180
QY	AFERTRRLRLREQRKALRELEADPRTATLTDIOKQVRQSQOLRVQVQBSAQILQSRLAETD	240
Db	181 AFERTRRLRLREQRKALRELEADPRTATLTDIOKQVRQSQOLRVQVQBSAQILQSRLAETD	240
QY	AFERTRRLRLREQRKALRELEADPRTATLTDIOKQVRQSQOLRVQVQBSAQILQSRLAETD	240
Db	181 AFERTRRLRLREQRKALRELEADPRTATLTDIOKQVRQSQOLRVQVQBSAQILQSRLAETD	240

OY 241 RHFLAGVASISERLK-----GKIHENL 264
 Db 241 RHFLAGVASISERASRPNGPSPPADPYGRLHCGL 280
 RESULT 4
 AAM88857
 ID AAM88857 standard; Protein; 123 AA.
 XX
 AC AAM88857;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen SEQ ID NO:16450.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 XX
 OS cytosolic; gene therapy; vaccine; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PE 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225265.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227183.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0233398.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0233400.
 PR 14-SEP-2000; 2000US-0233401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241121.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0244674.
 PR 08-NOV-2000; 2000US-0244675.
 PR 08-NOV-2000; 2000US-0244676.
 PR 08-NOV-2000; 2000US-0244677.
 PR 08-NOV-2000; 2000US-0244678.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.

17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251888.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
DR N-PSDB; AAK61638.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Claim 11; SEQ ID NO 16450; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
XX
SQ Sequence 123 AA;
Query Match 25.3%; Score 634; DB 22; Length 123;
Best Local Similarity 96.7%; Pred. No. 5e-47;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 288 QDIHPALTLDPGTAHQRLTISDCTIYAAGNLHPQLQDSPKRPDVSIVLSGSAFS 347
DB 3 RHFHPALTLDPGTAHQRLTISDCTIYAAGNLHPQLQDSPKRPDVSIVLSGSAFS 62
QY 348 SGVHYEVVVAEKTQVIGLAHEAASRKGSIOIOPSRGFICYMHGNGOVSACTEPTRL 407
DB 63 SGVHYEVVVAEKTQVIGLAHEAASRKGSIOIOPSRGFICYMHGNGOVSACTEPTRX 122
QY 408 N 408
DB 123 N 123
RESULT 5
ABG26213
ID ABG26213 standard; Protein; 735 AA.
XX
AC ABG26213;
XX

18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #26204.
DE
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
PN WO200175067-A2.
XX
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-0508631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS90400.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID NO 56572; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: the sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 735 AA;
Query Match 25.2%; Score 631; DB 22; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.3e-45;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 168 KSSTKSLRTTIGEAERLRLRLREROKAMLEADATRLTDEQVORYSOOLRRVOE 227
DB 598 KSSTKSLRTTIGEAERLRLRLREROKAMLEADATRLTDEQVORYSOOLRRVOE 657
QY 228 GAQILDERLAETDRHTFLAAGVASISELKKGIHETNTIYEDPFSKTYGLOTTIMSLF 287
DB 658 GAQILDERLAETDRHTFLAAGVASISELKKGIHETNTIYEDPFSKTYGLOTTIMSLF 717
QY 288 QDIHP 292
DB 718 QDIHP 722

RESULT 6
AAG89346
ID AAG89346 standard; protein; 500 AA.
XX
AC AAG89346;
XX
XX 11-SEP-2001 (first entry)
DE Human secreted protein, SEQ ID NO: 466.
XX
XX Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KM GENSET.
OS Homo sapiens.
XX
XX WO200142451-A2.
XX
PD 14-JUN-2001.
XX
XX 07-DEC-2000; 2000MO-IB0138.
XX
XX 08-DEC-1999; 99US-0169629.
XX
XX 06-MAR-2000; 2000US-0187470.
XX
XX (GENSET) GENSET.
XX
PI Dumas Mline Edwards J, Bougueleret L, Jobert S;
XX
XX WPI; 2001-367870/38.
DR N-PSDB; AAH64949.
XX
XX Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
XX diseases, and for diagnosis of those diseases -
XX
XX Claim 21; Page 913-914; 921pp; English.
XX
XX The invention relates to full length GENSET human nucleic acids encoding
XX potentially secreted proteins. The nucleic acids and the polypeptides
XX they encode may be used in the prevention, treatment and diagnosis of
XX diseases associated with inappropriate GENSET gene expression. For
XX example, they be used to treat disorders associated with decreased
XX GENSET gene expression by rectifying mutations or deletions in a
XX patient's genome that affect the activity of GENSET or by supplementing
XX the patient's own production of GENSET polypeptides. Conversely,
XX antisense nucleic acid molecules may be administered to down regulate
XX GENSET expression by binding with the cells' own genes and preventing
XX their expression. The sense and antisense nucleic acids may also be
XX used as DNA probes in diagnostic assays to detect and quantitate the
XX presence of similar nucleic acid sequences in samples, and hence to
XX determine which patients may be in need of restorative therapy.
XX The GENSET polypeptides may be used as antigens in the production of
XX antibodies and in assays to identify modulators (agonists and
XX antagonists) of GENSET polypeptide expression and activity. The
XX present sequence is a GENSET polypeptide of the invention.
XX
SQ Sequence 500 AA;
Query Match 24.5%; Score 613; DB 22; Length 500;
Best Local Similarity 31.6%; Pred. NO. 2.8e-44;
Matches 148; Conservative 83; Mismatches 222; Indels 16; Gaps 8;
QY 8 ELGSGICSTIYDVSIGCEHYFCRCITTEHWVQEOAGDCPRCRTFAPALAPSLK 67
DB 38 ELKCPICNDWFRDPLMISCGHNFECACIQDFWRLOAHE--TFCEPKMLCOYNNCTFNPV 95
QY 68 LANIVERSSEPLDALINARRARPCQAH-DKVKLFCTLDRALCFCEDEPALH--EQHO 124
DB 96 LDKLVKIKKRLP-----LKGHQCPBHGKGNLFLSPBDKILCFCKDKRLISGQCKE 149
QY 125 VTGIDDAFDELQRLKQQLALQDSEBHTFALQILKRLQALETSSTKSLRTTIGEAER 184
DB 150 FLQISDAVHFEMELAIQCGOLETTLKEQLTLRNMOKEALIAHKNKHLHQHVSMEELK 209

QY 185 LHRLLEROKAMELEADPTARTLDDIEQKVOYRSQOLRRVQAGQILQERLAEEDRHF 244
DB 210 LHOFLSKKEKEDILTELREBQKALNEMEMNLSQLAQCLLAKMDLVSIQAKTEQONSFPF 269
QY 245 LAGVASLSERLKG--KIHT-NLTYDEFTSKYTGLOTTINKSLFQDIHPVPAALTDLP 301
DB 270 LKDITTLHSLDQGMKVLATRELISRKLNGLGQKGIQYVWREMODTLCPSLPLTDP 329
QY 302 GTAHORLILSDCTIYAAGNLHPQLQDSPKRPDVSVIAGSFASSGVHYEVVAEKT 361
DB 330 KTAHPVLVLSKQTSVWMDI-KKIMPDPPEFDDSSVANVLSRGFTSGKWTVEVEYAKT 388
QY 362 QWVIGLAHPASRKSGSIQIOPSRGFCYVMHDGNDYSACTEPWRLNVRKLDKGVFLD 421
DB 389 KWTGVGVRESIIRKSGCPLTPGQFWLRLRNQTDLKALDLPFSLTLLNNLDKGIYLD 448
QY 422 YDQGLIEFNADMSWLYTFREKFPKLCSTYSPQSHANGKNVQPLRI 470
DB 449 YEGGQLSEFNAKTMTHTIYFSNTFMERKLYPFCPLDNGR-BNKEPLHI 496
RESULT 7
AAB43498
ID AAB43498 standard; protein; 580 AA.
XX
AC AAB43498;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human cancer associated protein sequence SEQ ID NO:943.
XX
XX Human; cancer associated gene; cancer antigen; detection; cancer;
XX diagnosis; cytostatic; proliferative; vulnereary; immunomodulator;
XX antidiabetic; antiaschematic; antirheumatic; antiallergic; antiviral;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
XX dermatologic; neuroprotective; thrombolytic; coagulant; nootropic;
XX vasotropic; antiporiatic; antiangiogenic; gene therapy; inflammation;
XX immune disorder; haematopoietic cell disorder; autoimmune disorder;
XX allergic reaction; graft versus host disease; organ rejection;
XX haemostatic; thrombolytic; cardiovascular disorder; infection;
XX neurological disease; drug screening.
XX
XX Homo sapiens.
XX
XX WO200055350-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000MO-US05882.*
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587533/55.
XX
XX N-PSDB; AAC77707.
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -
XX
XX Claim 11; Page 1506-1508; 2352pp; English.
XX
XX AACT7607 to AACT7448 encode the human cancer associated proteins given
XX in AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulnereary; immunomodulator;
XX antidiabetic; antiaschematic; antirheumatic; antiallergic;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
XX dermatologic; neuroprotective; cardiant; thrombolytic; coagulant;
XX nootropic; vasotropic; antiporiatic and antiangiogenic. The

CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and ABA44240 represent sequences used in the exemplification of
 CC the present invention.

XX Sequence 580 AA;

Query Match 23.4%; Score 583; DB 21; Length 580;
 Best Local Similarity 29.1%; Pred. No. 1.4e-41;
 Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;

QY 5 LDELICSLISLTYDPSVLSGCEHYPCRCITTEHWVROENAGARDCEPCRRFAEPALAP 64
 DB 77 LQOETTCPCYCLGYFAFAPMMLDCGNICACIACWGTAETNVS--CPQCEETFPQHMRP 134
 QY 65 SIKANIVRRYSFPLDAILNARRAP-----COAH-DKVALFCLTDRAALCFPC 114
 DB 135 NRIILANVTQ-----LVKQLRTERPSPGSGEMGVCEKHREPLKLYCEEDMPICVVC 185
 QY 115 DEPALHEOHVGTIDAFDELRELKDOLADDSREHTEALQLKRO-----LAE 166
 DB 186 DMSREHGHSVLPLEAVBGFKEQIQNL-----DLKRVKDLKRRRAQEQARAE 237
 QY 167 TRSSTKLRTTIGFAERLRLRLR---RQKAMLELE-----ADPA 205
 DB 238 LLSLQMEKEKIYWEERQYHSLKEHEYLRLARLEELDAIYNSINGAITQFCNSHLS 297
 QY 206 RLUTIDEQVORYSOOLKAVOBGAQLQERLAETDR-----HTPLAGV 248
 DB 298 SLIAQLEEKQOQPTREL-----LDIDIGTLISRAEKIRIRPEWITPDLQEKIHPAOKC 351
 QY 249 ASLSERLKGIHETNLTYEDEFTSKYTPLOVYIMRSLPQDHPV---PALTLDPGTAH 305
 DB 352 LFTLESLK-----QTEKMQSDMER--IQELBAQLISVDVILDPDTAT 393
 QY 306 QRLIISDDCTIYAGNLHROPLODSPKRFDEVESVLSSEAFSSGVHYWEVVAEKTQWT 365
 DB 394 PSLIISDNLROYAYSYLQ--QDLPDNERFNLFCVLSGPFINGRHYWEVEVDKAKWTI 452
 QY 366 GLAHEAASRKGSIQIOPSRGFCIYVHNDQYISACTEPWTRLVNRKLDKVGFLDIYDQ 425
 DB 453 GVCEDSVCKRGKGTSAPONGFMAVSLMYKREYVALTSPMTALPLRTPLORVGIFLDYDAG 512
 QY 426 LLIIFYNADMSMLYTF--REKFPGLKCSYFSPGSHANGKVVOPLR 470
 DB 513 EYSFYVWTERCHFTFTSHATFCGPVAPYFS--LISYGGKSADPLII 556

RESULT 8
 ABG97352
 ID ABG97352 standard; protein; 468 AA.

XX ABG97352;

XX 16-DEC-2002 (first entry)

DE Human CGDD3, INCYTE 3089944CD1.

XX Human; cell growth; differentiation; death; CGDD; cancer;
 KW cell proliferative disorder; arteriosclerosis; atherosclerosis;
 KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; porosis;
 KW polycythaemia vera; primary thrombocytopoenia; developmental disorder;
 KW renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;
 KW neurological disorder; Alzheimer disease; Parkinson's disease; asthma;

KW reproductive disorder; infertility; autoimmune disorder; gout; allergy;
 KW inflammatory disorder; acquired immunodeficiency syndrome; uveitis;
 KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;
 KW diabetes mellitus; glomerulonephritis; irritable bowel syndrome;
 KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
 KW rheumatoid arthritis.

OS Homo sapiens.

PN W0200272830-A2.

XX 19-SEP-2002.

XX 08-FEB-2002; 2002WO-US03715.

XX 09-FEB-2001; 2001US-26811P.

XX 23-FEB-2001; 2001US-271175P.

XX 08-MAR-2001; 2001US-274503P.

XX 09-MAR-2001; 2001US-274552P.

XX (INCY-) INCYTE GENOMICS INC.

PI Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR,
 PI Ding L, Xu Y, Gietzen KU, Tang TY, Lal PG, Duggan BM, Burford N;
 PI Lu DM, Richardson TW, Tran UK, Khare R, Walla NK;

DR MPI; 2002-723356/78.

DR N-PSDB; ABS78645.

PT New human proteins associated with cell growth, differentiation and
 PT death, useful for diagnosing, treating or preventing autoimmune or
 PT inflammatory disorders (e.g. AIDS, allergy or anemia), cancer,
 PT atherosclerosis or hepatitis

PS Claim 1; Page 144-145; 181pp; English.

XX The invention relates to an isolated polypeptide comprising CGDD1-12
 CC (cell growth, differentiation and death), a naturally occurring amino
 CC acid sequence at least 90% identical to CGDD, a biologically active
 CC fragment or an immunogenic fragment. Also included are the
 CC polynucleotides encoding CGDD1-12, a recombinant polynucleotide
 CC comprising a promoter sequence operably linked to the CGDD
 CC polynucleotides, a cell transformed with the recombinant polynucleotide,
 CC a transgenic organism comprising the recombinant polynucleotide, an
 CC anti-CGDD antibody, screening for compounds which bind to/modulate
 CC are and/or agonists of CGDD or alter the expression of CGDD
 CC polynucleotide and a CGDD polynucleotide microarray.

CC The polypeptides, polynucleotides, agonists and antagonists are
 CC useful for diagnosing, treating or preventing disorders associated with
 CC aberrant expression of CGDD, particularly cell proliferative (e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, porosis, primary
 CC thrombocytopoenia or cancer), developmental disorders (e.g. renal
 CC tubular acidosis, anaemia or mental retardation), neurological disorders
 CC (e.g. Alzheimer disease, Parkinson's disease or epilepsy),
 CC reproductive disorders (e.g. infertility or a disruption in the
 CC menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,
 CC (acquired immunodeficiency syndrome) allergies, asthma, autoimmune
 CC thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,
 CC glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis,
 CC osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis,
 CC uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic
 CC infections. They are also useful in the assessment of the effects of
 CC exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of proteins associated with CGDD. The present sequence
 CC represents a CGDD protein.

XX Sequence 468 AA;

Query Match 22.4%; Score 560; DB 23; Length 468;

Best Local Similarity 32.5%; Pred. No. 1e-39;
 Matches 154; Conservative 75; Mismatches 191; Indels 54; Gaps 16;

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Oy 1 MACSKDELGLSICLSIYQDPVSLGCEHYFCRCITTEHVQAEAGARDCEPCRRTPFAEP 60
Db 6 LSTNQEATCAICIDITFDPMWDCGHNFCRECRICRCWGP-E-GPYACPECRRLSPOR 63
Oy 61 ALASPLKLANIVERTSEFPDAIINARRARP-----COAH-DKVKLFCLTDALLCF 112
Db 64 NLRRNRLPKKAEH-----ARRLHPPSPVPGVCRAHREPLAFCGDELRLLCA 112
Oy 113 FCDEPALHEOHQVTCIDDAPELORELKDQLOALQDSREHTEALQLKROLAET---K 168
Db 113 ACERSGEHMAHVRPLQDAEDLAKLEKESLEHL---RKOMQDALLFOAQADEFCVLWQ 168
Oy 169 SSTRSLRTIGEARFERHLRLREKQKAMLELEADTARTLDIEKQVRYSOQLKRVGB 228
Db 169 KVESQKONVAGEERLRLRLAEERQQLRLKEELEVLRLRGAHLCQO----- 221
Oy 229 AOILQERLAETDRFTFLAGVASLSERLKG---KIHTNLTJEDFPTSKYTGPIQY-TIMK 284
Db 222 SAHLAELEAELEGGQOLPALGLDQ-IDALRRVODVLRPE-----VYPMELRTYCR 274
Oy 285 --SLFQDIHPVPALTLDPGTANORLIISDCTIYVAGNLHPQLQDSPKRPDEVSVYLG 342
Db 275 VPGIVETLRRERGVTLDPDTANPELILSEDRRSYORGLR-QALPDSPERFDPGCVLG 333
Oy 343 SEAFSSGVHYWEVYVAEKTQWVIGLAHEAASRKSGSIQIPSRGFYCIYMHGNOVSACTE 402
Db 334 QERTSGRHYYEVEVGDRTSMALGYCENVRNKEKEGELSGAGNEFILLVL-GSYNNSER 392
Oy 403 PWTRLNVRDKLDKYGVELDYDOGLLIIFYNADMSNLTYFRE-KEPGKLSYFSP 455
Db 393 ALAPL--RDPFRVGIFFLDYEAHLSFYSATDGSILFFPELPSGTLRPLESP 444

RESULT 9
AAR15148
ID AAR15148 standard; Protein: 475 AA.
XX AAR15148;
AC 14-FEB-1992 (first entry)
XX Ro/SSA autoantigen.
DE Autoantibody; autoantigen; SLE; systemic lupus erythematosus.
KM Homo sapiens.
XX OS
XX WO9117171-A.
XX PN
XX 14-NOV-1991.
XX PD
XX PF 07-MAY-1991; 91WO-US03139.
XX PR 07-MAY-1990; 90US-0520270.
XX PA (OKLA-) OKLAHOMA MED RES FO.
XX PI Frank MB, Itoh K;
XX WP1: 1991-353712/48.
XX DR N-PSDB; AAQ14798.
XX PT
XX DNA encoding an Ro-SSA autoantigen - useful for diagnosing
XX auto-immune disorders or presence of auto-antibodies
XX PS
XX Disclosure; Fig 2; 41pp; English.
XX
XX A CDNA library (from human thymus mRNA) in lambda gtl1 was screened
XX with serum from a patient having systemic lupus erythematosus. Two
XX clones were reactive with sera (from a panel of lupus patients)
XX which contd. autoantibodies against 52 kD protein.
XX Both the CDNA and the protein expressed from it, or portions of it,
XX are useful as diagnostic agents in the identification of patients

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CC having autoantibodies and in the identification and analysis of
CC the structural and functional properties of the autoantigen and for
CC application in immunotherapeutic regimens.
XX
SQ Sequence 475 AA:
Query Match 22.1%; Score 552.5; DB 12; Length 475;
Best Local Similarity 31.3%; Pred. No. 4,6e-39;
Matches 150; Conservative 88; Mismatches 208; Indels 33; Gaps 14;
Oy 7 DELGSLISLTIYQDPVSLGCEHYFCRCITTEHVQAEAGARDCEPCRRTPFAERLASL 66
Db 12 ERYTPICLDPEVEVSTECGHSFCQECISQ---VGKGGSVCPVCRQRLKLNLRNR 67
Oy 67 KLANIVERTSEFPDAIINARRARPQCOAH-DKVKLFCLTDALLCFPCDEPALHEOHQV 125
Db 68 QLANNVNMLKETSQA--REGTQGRCAVHGERLHFLFEKDGKALCWACAGSRKHHDAM 125
Oy 126 TGIDAFPELORELKDQLOALQDSREHTEALQ---LKROLAETKSTSLRTTIGENAF 182
Db 126 VPLEBAQEOYEKLOVALGEELR-RKQELAEKLEVEIAIKR--ADWKKTVEYOKSRTHAEF 182
Oy 183 ERLHRLREKQKAMLELEADTARTLDIEKQVRYSOQLKRVGBQQLQERLAETPRH 242
Db 183 VQKRFVLEEERQLOLEKEDREQLTGEKAKLAQO-----SQALEDLISELDRR 235
Oy 243 TFLAGVASLSERL--KGIHTNLTJEDFPTSKYTGPIQYTIWKSIFQD--IHVPALY 298
Db 246 CHSALLELLEQVIYLERSESNLKDITLITSELSVCHVPLKMLKATCAVH-----IT 290
Oy 299 LDPTANRRLIISDCTIYVAGNLHPQLQDSPKRPDEVSVYLGSEAFSSGVHYWEVYVA 358
Db 291 LDPTANRPLIISDQKQVRLEDITQ-QSIPGNEERFDSYPMVLGAQHPSGKHWEVDVT 349
Oy 359 EKTQWVIGLAHEAASRKSGSIQIPSRGFYCIYMHGNOVSACTEWPTRLNVRDKLDKYG 418
Db 350 GREAMDLYGCRDVSARKGHFLLSSKSGFWTTIWMKOKYTEGTYQTPHLQVPPCQVGI 409
Oy 419 FLVDYDOGLLIIFYN-ADMSNLTYFRE-KEPGKLSYFSPGOSHANGKRVQPLRINTVRI 475
Db 410 FLVDYAGWVSFYNIIDHOSLITYSFSECAFTGRLRPFSPG-FNQGKATPAULTLCPLNI 467

RESULT 10
ABP64866
ID ABP64866 standard; Protein: 485 AA.
XX ABP64866;
AC 25-FEB-2003 (first entry)
XX DT
XX DE Human protein SEQ ID 526.
XX KM
XX Human; expressed sequence tag; EST;
XX haematopoietic disorder; central nervous system disease; viral infection;
XX peripheral nervous system disease; non-healing wound; infectious disease;
XX immune deficiency; immune disorder; bacterial infection; allergy; cancer;
XX fungal infection; autoimmune disorder; congenital disorder; noctropic;
XX antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
XX immunostimulant; cerebroprotective.
XX KM
XX Homo sapiens.
XX OS
XX WO200259260-A2.
XX PN
XX 01-AUG-2002.
XX PD
XX 16-NOV-2001; 2001WO-US42950.
XX PF
XX 17-NOV-2000; 2000US-0714936.
XX PR
XX (HYSE-) HYSEQ INC.
XX PA

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XX Tang YT, Goodrich RM, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
XX WPI: 2002-590824/63.
DR N-PSDB; AB099452.
XX
XX New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity -
XX
PS Claim 20; SEQ ID 526; 394pp; English.

XX The present invention relates to novel human coding sequences
CC (AB099268-AB099608) and proteins (ABP64682-ABP65022). The sequences are
CC useful in therapeutic, diagnostic and research methods. The
CC polynucleotides may be used in the field of molecular biology as
CC hybridisation probes, primers for PCR, for chromosome and gene mapping,
CC for the recombinant production of protein, or in generation of anti-sense
CC DNA or RNA. The polynucleotides are useful in diagnostics as expressed
CC sequence tags (ESTs) for identifying expressed genes or for physical
CC mapping of the human genome. The proteins may be used as molecular weight
CC markers, or as nutritional sources or supplements. The proteins may be
CC used to maintain and expand cell population in a totipotent or
CC pluripotent state useful for re-engineering damaged or diseased
CC tissues, transplantation, manufacture of bio-pharmaceuticals or the
CC development of bio-sensors. The polynucleotides and proteins are useful
CC for preventing, treating or ameliorating disorders involving aberrant
CC protein expression or biological activity, e.g. haematopoietic disorders,
CC central/peripheral nervous system diseases, mechanical and traumatic
CC disorders, non-healing wounds, immune deficiencies and disorders,
CC infectious diseases caused by viral, bacterial or fungal infection,
CC autoimmune disorders, allergic reactions and conditions, coagulation
CC disorders, or cancer. The polynucleotide sequences of the invention were
CC assembled from ESTs isolated mainly by sequencing by hybridisation, and
CC in some cases, sequences obtained from one or more public databases.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pot_sequences.
XX

XX Sequence 485 AA:

Query Match 22.0%; Score 550.5; DB 23; Length 485;
Best Local Similarity 29.3%; Pred. No. 7e-39;
Matches 150; Conservative 94; Mismatches 181; Indels 87; Gaps 17;

XX 4 SIKDELICISITVDPSIGCEHYRCRJCIEHH-VHQEAGC-ARDPECKRTAEPA 61
DB 9 AIVEEACPTICMTFLREPMSTDCGHSCUSGLMEITGESONMGTCPLCAPVQPRN 68
XX 62 LAPSLKLANIVERSSFPDLATILNARRARPCQAH-DKVKLFCTIDTRALICFPDDEPALH 120
DB 69 LRPNNQLANVVEVRRLRLRHPGKLN--GDICRHEHCKMKPCKEVLLMCEACSSPEH 126
XX 121 EOHQVTDGIDAFDELQREIKDQALQDSEHTEALQILKROLAET-KSSTKSLRTTIG 179
DB 127 EASHVVPMEDEVMEYEMELHEALEHLK-KEQEEAMKLEVEGERKRTATWIKQVETRSQSIY 185
XX 180 EAFERHLRLREROKAMELEADTARTLIDIEQKQVRSQQR----KVQBEAQILQER 235
DB 186 WEFEKQRLLEKKQPPH-RQLGAEVAAALASIQREAAETMQKLELHNSLEIQQSOVLRM 244
XX 236 LAETDHTFLAGVASSERLKGKIHETNLTYEDFPSTSKYTGPIQYTIWKSIFQDI----- 290
DB 245 IAE-----LKERSQRRVR-----W-MLODIOEVLN 268
XX 291 -----HPVPAAL-----TLDPGTAHQRLISDCTIVAYG 320
DB 269 RSKSMELAQPEPISLELKTDCRVILGLREILKTYAADVRIDPDPAVSRLIYSEDRKRVHYG 328
XX 321 NLHAPOLDSPKRFDVEVSYLGSEAFSSGVHYWEVVAETQVAVIGLAHAAARKSGSIOT 380
DB 329 DTN-OQLPDNPERFYRYNTVLAGSQCISGRHYWEVEVGDSWGLGVCCKONVDRKEVYVL 387

XX 381 QPSRGFYCIYMHNDGNOYSACTEPTPRLNVRDKLDKGVFLDYDQGLLIFPNADM-SWIX 439
DB 388 SPHYGFWVIRLRKGNENYRAGTDEXPILSLPVPRRRGIFVDYLAHDISFTVNTDCSHIF 447
XX 440 TF-REKFPCKLCSYSPGOSHANGKNVQPLRI 470
DB 448 TFPRTYPPGRLPLPFSPCYXS-IGTNNTAPLAI 478

RESULT 11

XX AAM48396 standard; Protein; 485 AA.
XX
XX AAM48396;
XX
XX 13-MAY-2002 (first entry)
XX
XX Human SSA-56kDa protein.
XX
XX Human; SSA-56kDa; virucide; anti-HIV; immunosuppressive; dermatological;
KW antiinflammatory; hepatotropic; Ro/SSA-like protein; autoimmune disease;
KW systemic lupus erythematosus; SLE; Sjogren syndrome; RNA virus infection;
KW HIV infection; hepatitis B; hepatitis C; chronic pathogen infection;
XX transgenic animal.
XX Homo sapiens.

XX Key location/Qualifiers
XX Domain 16..54
XX /note="2inc finger domain"
XX Region 91..123
XX /label="B.Box
XX /note="Cysteine and histidine rich region"
XX 190..245
XX /note="Leucine zipper"

XX WO200188128-A1.

XX 22-NOV-2001.

XX 12-MAR-2001; 2001WO-FR00725.

XX 17-MAY-2000; 2000FR-0006315.

XX (ISTA-) ISTAC.

XX (INST) INST PASTEUR LILLE.

XX Bahr G, Cocude C, Capron A;

XX WPI: 2002-066692/09.
XX N-PSDB; ABA98677.

XX New human Ro/SSA-like polypeptide, useful for treatment, prevention and
PT diagnosis of e.g. autoimmune disease and viral infection, also related
PT nucleic acid and antibodies -
XX

PS Claim 1; Page 86-88; 109pp; French.

XX The present sequence is a novel human Ro/SSA-like protein, SSA-56 kDa.
CC The coding sequence for SSA-56 protein can be used for the diagnosis or
CC monitoring of autoimmune diseases (particularly systemic lupus
CC erythematosus, SLE, or Sjogren syndrome), infections by RNA viruses
CC (particularly HIV or hepatitis B and C) or chronic pathogen infections
CC associated with autoimmune manifestations. The coding sequence for SSA-56
CC protein can also be used to generate transgenic animals for studying the
CC aetiology of Ro/SSA-like protein-related diseases or effects of viral
CC infection on expression of Ro/SSA-like protein.

XX Sequence 485 AA:

Query Match 22.0%; Score 550.5; DB 23; Length 485;
Best Local Similarity 29.3%; Pred. No. 7e-39;


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Db      329 DNN-QKLDPNPERFRINIVLASQCLSSRRHWEEVGRSEKGLGVCKQNDKREYVTL 387
Oy      381 QPSRGFYCIYMDGNQYSACTEPWRLNVDKLVGVELDYDOGLIFYNADDM-SWLY 439
        388 SPHYGFWVIRLKGNEYRAGTDEYPLSLPVPFRARGIVDEYEAHDISFYNTYDGSNIF 447
Oy      440 TF-REKFPGLKLSYSPGQSHANGKNOPLRI 470
        448 TPRRYPFGRLPLYPSPCY5-IGTNTAPLAI 478

```

RESULT 13

AAE02616 standard; Protein; 516 AA.

AAE02616;

06-AUG-2001 (first entry)

Murine haematopoietic lineage switch (HLS)-5.

Murine haematopoietic lineage switch; HLS-5; tumour suppressor; cancer;

ring finger B-box coiled-coil; RBCC; transcriptional regulator; tumour;

acute myeloid leukaemia; drug screening; gene therapy; cytostatic.

Mus musculus.

Key Location/Qualifiers

Domain 36..75

Region 111..152

Region 219..266

Domain 368..507

WO200138374-A1.

31-MAY-2001.

24-NOV-2000: 2000MO-AD01439.

24-NOV-1999: 99AU-0004216.

(UYMA-) UNIT WESTERN AUSTRALIA.

Klinken SP, Lalonde J, Williams JH;

WPI; 2001-367663/38.

N-PSDB; AAD06777.

Novel tumor suppressor gene, HLS-5, useful for regulating cell growth

and treating a condition characterized by aberrant cell growth -

Claim 4; Page 101-102; 111pp; English.

The present invention relates to a tumour suppressor gene, termed

haematopoietic lineage switch (HLS)-5 and the protein it encodes.

HLS-5 is a member of ring finger B-box coiled-coil (RBCC) family of

transcriptional regulators. HLS-5 exhibits tumour suppressor activities

in acute myeloid leukaemia and breast cancer cells. HLS-5 DNA, protein

and its Ab are useful for treating a condition characterised by aberrant

cell growth. HLS-5 DNA and protein are useful to identify a substance

capable of affecting HLS-5 function, or capable of modulating cell

growth. HLS-5 DNA and protein sequences are useful for diagnosing and

treating tumours and cancers. HLS-5 polypeptides are also useful for

screening drugs for treating diseases. HLS-5 DNA is used in gene

therapy. The present amino acid sequence is murine HLS-5.

Sequence 516 AA:

Query Match 20 88; Score 520; DB 22; Length 516;
Best Local Similarity 30.28; Pred. No. 3.4e-36;
Matches 153; Conservative 79; Mismatches 214; Indels 60; Gaps 17;

```

Oy      4 SLKDELCSICSLIYDDPSLGCENFCRCRCHENHWROBAQARCCPECRFPAPALA 63
        29 SFKEELLCAYCIPFPFDATYLRGHNFCRCVSGC---EVQTPSPCPCKEAAVGEIR 85
Oy      64 PSIKIANIYERRSSFPID-AILNARRAPCOAH-DVKVLCITLDALCFPCDEPALHE 121
        86 THTLNNLVETTLREAEAGARWTRSPRCRAHRAPLTFLCEDEKELLCQAQADARRQ 145
Oy      122 QHOYTGIDAFDELQELKDQLADQSERENHEALQLKQLAEKSSKSLRT---- 177
        146 EHRVOPIKDPAODFRAKCKMHEVL---REKAKAFWALRKY-FAIAKHNEVQTTWLG 200
Oy      178 -IGEAERLRLRLREKOKAMLELEADTARTLDIOKORYSQOLRKVOEGAOITQERL 236
        201 RINDERDKLDFLVEEQATLDMKKESSKKHQAEEKMKQLEOTBALARETERLOMEK 260
Oy      237 AETDRHTFLAGVASLSERLGKIHTNLTAYEDP-----TSKYTGPLQYTIKSLRQ 288
        261 KEDDM-TPLMKHKSRRRL-----FCYEPAPLQPLMDACKTLESIQYRWKRMKG 312
Oy      289 DIHPVPAALTLDPGTAHQRLISDCTIYAGMLHPQPLDSPKRDVEYSVLGSAFSS 348
        313 SVESVP--FSLDPTAGWLKADDLTSVINSGRYQ--VENPERSSAPCLLGSOVFSK 368
Oy      349 GVHYWEVYVAEKQWYGL---AHBAASRK-----SIQIPSRGFCIVMHDGN 395
        369 GSHSMEVDVGGLEPTMRGVVRYOAHQAQADVGGEGSHSHCYHDTRSQFWLCKTQGV 428
Oy      396 QYSAC-----TEPWRNLNVDKLVGVELDYDOGLIFYNADDMSWLYTFREKPPGKL 449
        429 DGDCHTSDTATAPLVQAMPR---RLRVLECEBEGELSYDSEBRCHELTTFANH-GEV 483
Oy      450 CSTSPGQSHANGKNOPLINTVRI 475
        484 RPYFYLGASRGDP-PEPLRICHRLV 508

```

RESULT 14

AAE95331 standard; Protein; 488 AA.

AAE95331;

26-JUN-2001 (first entry)

Human protein sequence SEQ ID NO:17601.

Human; primer; detection; diagnosis; antisense therapy; gene therapy.

Human sapiens.

EP1074617-A2.

07-FEB-2001.

28-JUL-2000: 2000EP-0116126.

29-JUL-1999: 99JP-0248036.

27-AUG-1999: 99JP-0300253.

PR 11-JAN-2000: 2000JP-0118776.

PR 02-MAY-2000: 2000JP-0183767.

PR 09-JUN-2000: 2000JP-0241899.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Satto K, Yamamoto J;

Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

WPI; 2001-318749/34.

PR 10-JUL-2001; 2001US-304354P.
 PR 31-JUL-2001; 2001US-309198P.
 PR 16-AUG-2001; 2001US-312903P.
 PR 10-SEP-2001; 2001US-318462P.
 PR 12-SEP-2001; 2001US-318770P.
 PR 27-SEP-2001; 2001US-325430P.
 PR 27-SEP-2001; 2001US-325681P.
 PR 18-OCT-2001; 2001US-330380P.
 PR 31-OCT-2001; 2001US-335301P.
 PR 14-NOV-2001; 2001US-332172P.
 PR 14-NOV-2001; 2001US-332272P.
 PR 14-NOV-2001; 2001US-333184P.
 PR 14-NOV-2001; 2001US-333272P.
 PR 21-NOV-2001; 2001US-332094P.
 PR 03-DEC-2001; 2001US-337426P.
 PR 03-DEC-2001; 2001US-338092P.
 PR 04-DEC-2001; 2001US-337185P.
 PR 03-JAN-2002; 2002US-345705P.
 PR 08-MAR-2002; 2002US-0093463.

(CUBA-) CUBAGEN CORP.

PI Rastelli L, Mezes PD, Smithson G, Guo X, Gerlach V, Casman SJ;
 PI Boldog FL, Li L, Zehusen BD, Tchernov VT, Gangoli EA,
 PI Vermet CAM, Pena CE, Burgess CE, Liu X, Spytek KA, Gorman L,
 PI Spaderna SR, Voss EZ, Malayankar UM, Anderson DW, Patturajan M,
 PI Miller CE, Taupier RJ, Padigar M, Shenoy SG, Kerkuda R, Gusev VY,
 PI Pochart PF, Zhong M;

XX WPI: 2002-732824/79.
 DR N-PSDB; ABV99363.

PT New NOVX polypeptides and polynucleotides, useful for preventing,
 PT diagnosing or treating NOVX-associated disorders e.g. diabetes, cancer,
 PT Alzheimer's disease, dyslipidemias, obesity, immune or hematopoietic
 PT disorders, and asthma

XX Claim 1; Page 142-143; 619pp; English.

XX The present invention relates to new isolated proteins (NOVX) and their
 CC coding sequences (ABV99327-ABV99595 and ABP70049-ABP70149), where X is
 CC any number from 1 to 48. The NOVX proteins and coding sequences are
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, preferably a NOVX-associated disorder.
 CC The NOVX coding sequences and proteins are useful for treating,
 CC preventing or diagnosing diseases such as metabolic disorders, diabetes,
 CC obesity, infectious disease, anorexia, cancer-associated cachexia,
 CC cancer, neurodegenerative diseases, Alzheimer's disease, Parkinson's
 CC disease, immune disorders, hematopoietic disorders, cardiovascular
 CC disorders, fertility, bronchial asthma, AIDS, dyslipidemia, metabolic
 CC disturbances associated with obesity, metabolic syndrome X or wasting
 CC disorders associated with chronic diseases or various cancers. The NOVX
 CC coding sequences and proteins may also be used as targets for the
 CC identification of small molecules that modulate or inhibit e.g.
 CC neurogenesis, cell differentiation, cell proliferation, hematopoiesis,
 CC wound healing and angiogenesis, in gene therapy, in generation of
 CC antibodies that bind immunospecifically to NOVX substances for use in
 CC therapeutic or diagnostic methods.

XX Sequence 4675 AA;

Query Match 19.9%; Score 499.5; DB 23; Length 4675;
 Best Local Similarity 27.2%; Pred. No. 5.7e-33;
 Matches 166; Conservative 68; Mismatches 187; Indels 189; Gaps 18;

OY 1 MACSLDELICSTICLSITDPPVSLGCEHYFCRCITEHWYRQAGARDCPECRTFAEP 60
 DB 4076 LSTNIQEEATYCAICLDYFTDPVMTDCGHFRCRCIRCMQPE--GPYACPECRELSPPQR 4133
 OY 61 ALAPSLKLANIVRYSSFLDALINARBARP-----COAH-DKYKLFCLDRALLCF 112
 DB 4134 NIKNPRLAKMAEM-----ARRLHPSPVPQGVCPARREPLAFCGDELRLCA 4182

OY 113 FCDEPALHROHQVGTIDDAFDELQKQALQADSERRETEALQILKQALAE-----K 168
 DB 4183 ACERSEHNHARVRPQDAEDKAKLEKSLHEIL-----RQMDALLFQAQADETCVLMQ 4238
 OY 169 SSTKSLRTTIGAFEPFLHRLRE-----RQKAMLEELBADTARFL----- 208
 DB 4239 KWEISORONVLTGFEFLRLILABGCTAANAAGEEELKQSAHLAEILIAELERLPAPACAG 4298
 OY 209 -----TDIEKQRYRSGQLRKYQEGQILIGERLAETDRH 242
 DB 4299 AAGSEFPMCGLSLSRPPEGVFPKCTPKPEPDALACAMR-----QGCQVDEPTMIQ 4352
 OY 243 TPLAGVASLSERLKGRIHETNLTYEDEPYSKYTG---LQYTIWK-----SLFQDIH 291
 DB 4353 MWLGFAQGVTLTPASGAQONI-----SPGTGSMFRLSFLFKYKCSQSAITRMVH 4405
 OY 292 -----PVPA----- 296
 DB 4406 TVPKTRPCRGQSPPLPPSPAPAPAGLVTATTCFQMTPGVGRPPQDIKALRRYQVYK 4465
 OY 297 -----LTLDPGAHQRLLTSDCTIVAYGNLHPQ 326
 DB 4466 LQPEVYPMELRTVCYRPGIVETLRRRGCDVTLDPDTANBELTISEDRNSVQNGDLR-QA 4524
 OY 327 LQSPKRFVENVSLGSEAFSSGVHYWEVVAEKTOVIGLAHEAASRKGSIOIPSRCF 386
 DB 4525 LPDSPERFDGPCVLQGERETSGRHWYWEVGDRTSMALGVCHENNRREKGLSANGN 4584
 OY 387 YCIYMDGNQYSACTEPWTRLNVRKDKKGVGLDYDQCLILTYNADNDSWLYTFRE-KF 445
 DB 4585 WILVFL-GSYNNSERALAPL--RDPFRVGIPLDYEAGHLSPYSATDGLTFPFETDP 4641
 OY 446 PGKICSYFSP 455
 DB 4642 SGTLRLPLFP 4651

Search completed: October 7, 2003, 17:48:14
 Job time: 88 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 17:45:31 ; Search time 42 Seconds

(without alignments)
1087.622 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELCSICLSITYQD.....GOSHANGKNVQPLRIWVRI 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	778	31.1	624 2	S28418 probable zinc-bind
2	763.5	30.5	609 2	A43906 nuclear phosphopro
3	663.5	26.5	518 2	JC7387 testis-abundant fl
4	583	23.3	513 1	TVHURF ret finger protein
5	572	22.8	506 2	S37583 RING finger protein
6	552.5	22.1	475 1	A37241 52k autoantigen Ro
7	472.5	18.9	477 2	JE0343 tetr protein - rat
8	372.5	14.9	667 2	T09482 ring finger protei
9	370.5	14.8	438 2	T12494 hypothetical prote
10	364.5	14.6	667 2	T09013 RING finger protei
11	353.5	14.1	442 2	A57041 transcription regu
12	341	13.6	630 2	A49656 estrogen-responsi
13	304.5	12.2	634 2	I49642 estrogen-responsi
14	301.5	12.0	526 2	A37821 butyrophillin - bov
15	293	11.7	526 2	S70587 butyrophillin precu
16	286.5	11.4	487 2	S65133 butyrophillin - mou
17	276.5	11.0	365 2	A30891 regulatory protein
18	259	10.3	551 2	JC7562 translastoma RING
19	258.5	10.3	801 4	TVHURE glutafastoma RING
20	239.5	9.6	210 2	T28135 butyrophillin 1, B
21	233	9.3	150 2	T28135 butyrophillin 2, B
22	227	9.1	224 2	T28135 butyrophillin 2, B
23	224	8.9	792 2	T00082 ring finger B-box
24	213.5	8.5	638 2	JC7753 ring finger B-box
25	166.5	6.6	588 2	A49618 probable ataxia-te
26	161.5	6.4	331 2	T31998 hypothetical prote
27	161	6.4	698 2	T32840 hypothetical prote
28	158	6.3	375 2	T33778 protein C39F7.2 [1
29	158	6.3	375 2	F88947

30	155.5	6.2	574	2	S28275	hypothetical prote
31	155.5	6.2	974	2	E88549	protein F54G8.4 [1
32	145.5	5.8	412	2	D88072	protein ZK1240.1 [1
33	145.5	5.8	808	2	T22363	hypothetical prote
34	142.5	5.7	675	2	T01112	photomorphogenesis
35	140.5	5.6	1812	2	I49350	breast/ovarian can
36	137.5	5.5	700	2	A61527	stomach toxin beta c
37	137	5.5	487	1	DDBY18	DNA repair protein
38	133.5	5.3	560	2	A40044	PM1.1 protein - hu
39	133.5	5.3	589	2	A60198	PM1 protein, splic
40	133.5	5.3	589	2	S42517	PM1 protein, splic
41	133.5	5.3	589	2	S42381	PM1 protein, splic
42	133.5	5.3	593	2	B40045	probable transcrip
43	133.5	5.3	633	2	S19244	gene MY1 protein -
44	133.5	5.3	641	2	A40045	probable transcrip
45	133.5	5.3	802	2	S42518	PM1 protein, splic

ALIGNMENTS

RESULT 1
S28418
probable zinc-binding protein - Iberian ribbed newt
C/Species: Pleurodeles waltlil (Iberian ribbed newt)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000
C/Accession: S28418; S29476
R: Bellini, M.; Lacroix, J.C.; Gall, J.G.
EMBO J. 12, 107-114, 1993
A/Title: A putative zinc-binding protein on lampbrush chromosome loops.
A/Reference number: S28418; MOID:93154311; PMID:7679068
A/Accession: S28418
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-624 <BEL>
A/Cross-references: EMBL: L04190
R: Bellini, M.; Lacroix, J.C.; Gall, J.G.
submitted to the EMBL Data Library, October 1992
A/Reference number: S29476
A/Accession: S29476
A/Molecule type: mRNA
A/Residues: 1-263, 'LK', 266-624 <BE2>
A/Cross-references: EMBL: L04190; NID: g213867; PID: g213868
C/Comment: This DNA-binding phosphoprotein is enriched in nuclei of adult brain cells
C/Superfamily: Xenopus nuclear phosphoprotein knf; RING finger homology
C/Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:158-207/Domain: RING finger homology <RNG>

Query Match 31.1%; Score 778; DB 2; Length 624;
Best Local Similarity 35.6%; Pred. No. 5e-41;
Matches 171; Conservative 81; Mismatches 193; Indels 36; Gaps 9;

QY 7 DELGSLICISIVDDPSLGEHFCRCITHEHVRQAGARQCPGRRFAPALPSL 66
DB 158 EDTFCPLCRSLFEPVILCEGHNFCRCHIDKSW--ESASAFSCPECKEVLTKRYTNR 214
QY KLANIVERYSSPFLDALILNARRARPCQAH-DKYKLCFLTRALLCFECDEPALRHOQV 125
DB 215 VLANIVKKAAGVKDQVDRK---EKCDDEDEKLKFCRKGDTLACVICKSLHSNHF 271
QY 126 TGDDAFDELQREKQLOAL-----ODSERHTEALQLKROLAETKSSSTKSL 174
DB 272 LPIDAVG---YRQDLIALVPLETTMKENQKLCQDSQKSLHRENIIVDCKHIEC- 326
QY 175 RTIGGFERHLRLRROKAMELEADPARFLTDEQVQRYSOQLRVOGSAQILOE 234
DB 327 -----EERLHDFLREKAKWEDLNAERGLKDEANLVKWTQDCEIEAISTQS 380
QY 235 RLAEQDRHTFLAGVASERL-----GKTHETVLTEDPPTSKYTGSLQYTIWKSFLQD 289
DB 381 RLNESDPIALVLTDKISTEKCEHKGVAESVLYVKEISQGFNFGLQYTIWKEIKSV 440
QY 290 IHPVPAALTLDPGTARQLILSDCTIVAYGNLHPOPLQDSPKRFVDSVLSSEAFSSG 349

```

Db      441 VQPLAPLPLDLPNTAHPLVLESEGILTSVKTPTDT-KQQLPDNKRKRSQCLIVLAGAGFDSG 499
      350 VHYEVVVAEKTQWVIGLAHEAASRKSIOIQPSRGFYCIYVHDNGYSACTEPWTRLVN 409
      500 KHYEVEVGNKTAMVDYGMASSESSNRKGIKILPNKNGYVAIWLRCNGNAFALSPSTLNL 559
Oy      410 RDKLDKGVNPLDYDOGLLIFYNADMSWLYTFRKFPKLCYFSPGOSHANGKNVQPLR 469
      560 TSKPESKIGVLDYDEGGVSYFNADMSPLYTFNGSFTEKLYPLSLD-SGKNAEPLK 618
Db      470 I 470
      619 L 619

```

RESULT 2

```

A:Accession: A43906
A:Gene: knf7
A:Molecule type: mRNA
A:Residues: 1-609 <RED>
A:Cross-references: EMBL:M63705; NID:g214914; PID:g214915
A:Note: sequence extracted from NCBI backbone (NCBIN:64515, NCBI:64520)
C:Genetics:
C:Superfamily: Xenopus nuclear phosphoprotein knf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
C:Title: The cloning and characterization of a maternally expressed novel zinc finger nu
A:Reference number: A43906; MUID:92038424; PMID:1936552
A:Accession: A43906

```

```

Query Match      30.5%; Score 763.5; DB 2; Length 609;
Best Local Similarity 35.4%; Pred. No. 3,9e-40;
Matches 167; Conservative 88; Mismatches 200; Indels 17; Gaps 9;

```

```

Oy      7 DELLSICLSIYQDPVSLGCEHYFCRCRTEHWVQEAQADCECHRTFAEPALPSL 66
      141 EELNCPICLVELFKDPVWVACGHNFCRSCIDKAW---EGSSPACCECHRESTIDRKYTNR 197
      67 KLANIVERYSFPLDAILNARARPCQAND-KYKLECLTDALCFCDPEALHEOHV 125
      198 VLANLAKKAACCTPVTPVEKTRPLEKCESEHDERLKYCKDGTLSVCVCRDLSLKAHSNF 257
Oy      126 TGIDDAFDELQRELKDOALODSERHEALQLKRLAETKSTKSL---RTTIGRAF 182
      258 LPIDAVGVYREEASATAPLEASLKV-TE--QLSSESDKTEQHNKMSQYKEHITSEF 314
      183 ERLRLRLEROKAMLELEADTARTLIDEQKQVRSQQLRRVQGAQILDERLAETDRH 242
      315 EKLKFLEREREKLELOLKEGSENLITMENNLVYMOSDAIKTTISLAERMDTISI 374
Oy      243 TFL---AGVASLSERLKGITHEFN-LTYEDEFPSKYTPLOLYTWSLFDIHVPAL 297
      375 SFMLDIKAFIDKCOEQRAVISTGNTLLSKELCQSTFGPIQIYIMKELKSLVJPSLPM 434
Oy      298 TLDDGTIAHQRLILSDCTIVAGNLHPQLODSPRRFVEVSVLGSEAFSSGVHWYV 357
      435 LLDPTSAHPNLHLSDELTSVRGE-NKLSTLPDNPFRFQSCILVLSQGFDSGRHWYEV 493
Oy      358 AEKTQWVIGLAHEAASRKSIOIQPSRGFYCIYVHDNGYSACTEPWTRLVNROKLDKVG 417
      494 GDKRAMVDYGMASSESSNRKGIKILPNKNGYVAIWLRCNGNAFALSPSTLNL 553
Oy      418 VFLDYDOGLLIFYNADMSWLYTFRKFPKLCYFSPGOSHANGKNVQPLR 469
      554 VYVDYEGGQISFYNADMSWLYTFRKFPKLCYFSPGOSHANGKNVQPLR 604

```

```

RESULT 3
JC7387
testis-abundant finger protein - human
C:Species: Homo sapiens (man)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7387
C:Accession: A.; Yamagishi, T.; Tomiwa, N.; Yamauchi, Y.; Hishinuma, T.; Okada, K.; Suz
Biochem. Biophys. Res. Commun. 276, 45-51, 2000
A:Title: Molecular cloning of testis-abundant finger protein/ring finger protein 23 (
A:Reference number: JC7387
A:Contents: Testis
A:Accession: JC7387
A:Molecule type: mRNA
A:Residues: 1-518 <OR>
A:Cross-references: DBJ:AB046381
C:Comment: This protein, a member of the ring-B box-coiled coil-B30.2 protein family,
C:Genetics:
A:Gene: tfp
A:Map position: 6p21.3-6p22.1
A:Insertions: 151/3; 183/3; 260/3; 268/2; 298/2; 337/1
C:Superfamily: tfp transforming protein; RING finger homology
C:Keywords: coiled coil; testis

```

```

Query Match      26.5%; Score 663.5; DB 2; Length 518;
Best Local Similarity 32.8%; Pred. No. 5.5e-34;
Matches 167; Conservative 85; Mismatches 196; Indels 61; Gaps 13;

```

```

Oy      4 SLKDELCSICLSIYQDPVSLGCEHYFCRCRTEHWVQEAQADCECHRTFAEPALPSL 61
      22 NQGVASCSVCLIEYKEVYITICGHNFCRSCIDKAW---RDFPCVCKTSRTSR 77
Oy      62 LAPSLANIVERYSFPLDAILNARARPC-QANDKVKLECLTDALCFCDPEALH 120
      78 LRPNQLDSWVE-IAKOLQAVKRIKIDESCIPQHHEALSLFCYDEQEAVALICASHH 135
Oy      121 EGHQVYTGIDDAFDELQRELKDOALODSERHEALQLKRLAETKSTKSLTTTGE 180
      136 RPHIVPLDDATQVEKELQKLEPLEKLEITRKESSEKRPDELRLVSRQQLR 195
Oy      181 AFERLRLRLEROKAMLELEADTARTLIDEQKQVRSQQL-----RK 224
      196 EEEELHRLDEEQVLLRLREE---QDILQRLRENAHAGDKRRDLAHLAEVEKC 251
Oy      225 VQGAQILQERLAETDRH---TFLAGVASLSER---LKGITHEFNLTYEDEFPSKYTG- 276
      252 LOSGCEHMLKDVSTLEKNIPKRFSGSLSTICPRDHRKALLGLVKEIN-RCEKVKTEVTSV 310
Oy      277 -----PLQY---TIMKSLFDIHVPALTLDDPGTAHQRLILSDCTIVAGN 321
      311 STELEKNFSNFPROYFALRKILKOLIAVY-----TLDPETHAPNLVLSERKSVKFE 363
Oy      322 LHPQLODSPRRFVEVSVLGSEAFSSGVHWYEVVVAEKTQWVIGLAHEAASRKSIOIQ 381
      364 TRLRLPLPTPRFTTYPCVLAETGTSGRHWYEVGKTHANGVCDVSRRGELPPL 423
Oy      382 PSRGFYCIYVHDNGYSACTEPWTRLVNROKLDKGVNPLDYDOGLLIFYNADMSWLYTF 441
      424 PETGYWVRVLMNGDKRYAATTPRPPLHLYKVPKRGVIFLDEAGLSTYNTDASHITF 483
Oy      442 REKFPKLCYFSPGOSHANGKNVQPLR 470
      484 TDTFTKLMPLFPYPG-IRAGGRNAPLTI 511

```

RESULT 4

```

TYHURP
ret finger protein - human
N:Alternate names: transforming protein tfp
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 19-Jan-2001
C:Accession: A28101
R:Takahashi, M.; Inaguma, Y.; Hial, H.; Hirose, F.

```


Mol. Cell. Biol. 8, 1853-1856, 1988
 A:Title: Developmentally regulated expression of a human "finger"-containing gene encode
 A:Reference number: A28101; MUID:88246464; PMID:3380101
 A:Accession: A28101
 A:Molecule type: mRNA
 A:Residues: 1-513 <TAK>
 A:Cross-references: DDBJ:J03407; NID:g337371; PIDN:AAA36564.1; PID:g337372
 C:Genetics:
 A:Gene: GDB:RFP
 A:Cross-references: GDB:511359; GDB:1391662
 A:Map position: 6p22-6p21.3
 C:Superfamily: rfp transforming protein; RING finger homology
 C:Keywords: DNA binding; transforming protein; zinc finger
 F:1-315/Product: transforming protein rfp (fragment) #status predicted <RET>
 F:12-62/Domain: RING finger homology <RNG>
 F:16-127/Domain: metal and nucleic acid binding #status predicted <TMN>
 F:16-56/Region: zinc finger C3HC4 motif

Query Match 23.3%; Score 583; DB 1; Length 513;
 Best Local Similarity 29.1%; Pred. No.5.7e-29;
 Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;

```

OY 5 LKDELCSICLSIYODPVSLGCEHYFCRCITEHWVROAOGARDCPECRFPAPALAP 64
DB 10 LQGETTCPCLOYFVPMMLDCGHNCCACIARCMGTAETNS--CPQCRRETPQNHMR 67
OY 65 SKLANIYERYSFPLDALIMARRAAR-----COAH-DKVKLFCLTRALLCFCFC 114
DB 68 NHILANVTQ-----LVKQLRTERPSGCGEMGVCEKHREPLKLYCEBODMPICVVC 118
OY 115 DEPALHEOHQVYGDAPFELQELKDQALQDSREHTEALQILKRO-----LAE 166
DB 119 DSRREHGHSVLPLEAVBGFKEQIONRL-----DHILKRVKDLKRRRAOGEQARAE 170
OY 167 TKSSTKSLTPTTIGEAERLRLRLEROKAMLELEADTAETLTDIEQVORYS----- 219
DB 171 LLSLQMEREKIYWEFEQLYHSLKEHEHYLLARLELDALAYNSINGAITQSCNISHLS 230
OY 206 RFLVTDIEOKVORYSOOLRVQDSGAOTLOERLAETDR-----HFFLAGVASLSER 254
DB 231 SLIAOLEERQOQPTREL-----LDIDGTLRSRAERIRIPERWITPRDQEKIHFAQK 283
OY 249 ASLSERLAKKIHETNLTVDFTSKYTGLOTTIKSLFQDINHVP---PALTLDPGTAH 311
DB 285 LFLTESLK-----OPTERKQSDMER--IOELREAOQVSDVTLDPDAVPSLILS 325
OY 306 ORLLISDDCTIYAVGNLHPQLDPSKRPDVEVSLGSEAFSGVHYWEVVAEKTOWI 365
DB 327 PSLILSDNLQVRYSTIQ-QDLRPNPERNLFPVLSGSCFAGRIHYWEVEGDKAKMTI 385
OY 366 GLAHEAASRKGSIQIQPSRGFYCIYVHDGNOYSACTEPWTRLNVNRDKLDKGVFLDYDOG 425
DB 386 GVCEDSVCKRGVTSAPQNGFMAVSLMYGKEYWALISPTALPLRLRPLQRVGIFLDYDAG 445
OY 426 LLIFVADMSWLYTF-REKFPGLKCSYSPGOSHANGNVOPRLI 470
DB 446 EVSFFNVTERCHTFEFSHATFCGPVAPYFS--LSYSGKSAAPLII 489

```

RESULT 5
 S37583
 RING finger protein rfp - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S37583
 R:Takehashi, M.
 submitted to the EMBL Data Library, October 1993
 A:Reference number: S37583
 A:Accession: S37583
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-506 <TAK>
 A:Cross-references: EMBL:X75343; NID:g406747; PIDN:CAA53092.1; PID:g406748

C:Superfamily: rfp transforming protein; RING finger homology
 C:Keywords: zinc
 F:5-55/Domain: RING finger homology <RNG>

Query Match 22.8%; Score 572; DB 2; Length 506;
 Best Local Similarity 28.5%; Pred. No.2.7e-28;
 Matches 148; Conservative 88; Mismatches 190; Indels 94; Gaps 14;

```

OY 5 LKDELCSICLSIYODPVSLGCEHYFCRCITEHWVROAOGARDCPECRFPAPALAP 64
DB 3 LQGETTCPCLOYFVPMMLDCGHNCCACIARCMGTAETNS--CPQCRRETPQNHMR 60
OY 65 SKLANIYERYSFPLDALIMARRAAR-----COAH-DKVKLFCLTRALLCFCFC 114
DB 61 NHILANVTQ-----LVKQLRTERPSGCGEMGVCEKHREPLKLYCEBODMPICVVC 111
OY 115 DEPALHEOHQVYGDAPFELQELKDQALQDSREHTEALQILKRO-----LAE 166
DB 112 DSRREHGHSVLPLEAVBGFKEQIONRL-----DHILKRVKDLKRRRAOGEQARAE 163
OY 167 TKSSTKSLTPTTIGEAERLRLRLEROKAMLELEADTAETLTDIEQVORYS----- 219
DB 164 LLSLQMEREKIYWEFEQLYHSLKEHEHYLLARLELDALAYNSINGAITQSCNISHLS 223
OY 220 -----QOLRVQDSGAOTLOERLAETDR-----HFFLAGVASLSER 254
DB 224 GLIAOLEERQOQPTRELDDIDGTLRSRAERIRIPERWITPRDQEKIHFAQKPLTES 283
OY 255 LKGIHETNLTVDFTSKYTGLOTTIKSLFQDINHVP---PALTLDPGTAHOLILS 311
DB 284 LK-----OPTERKQSDMER--IOELREAOQVSDVTLDPDAVPSLILS 325
OY 312 DDCTIYAVGNLHPQLDPSKRPDVEVSLGSEAFSGVHYWEVVAEKTOWIYGLAHEA 371
DB 326 DNLQVRYSTIQ-QDLRPNPERNLFPVLSGSCFAGRIHYWEVEGDKAKMTI 384
OY 372 ASRKGSIQIQPSRGFYCIYVHDGNOYSACTEPWTRLNVNRDKLDKGVFLDYDGLIFYN 431
DB 385 VCKRGVTSAPQNGFMAVSLMYGKEYWALISPTALPLRLRPLQRVGIFLDYDAGEVSFYN 444
OY 432 ADDMSWLYTF-REKFPGLKCSYSPGOSHANGNVOPRLI 470
DB 445 VTERCHTFEFSHATFCGPVAPYFS--LSYSGKSAAPLII 482

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RESULT 6
 A37241
 52k autocantigen Ro/SS-A - human
 N:Alternate names: Sjogren syndrome antigen A
 C:Species: Homo sapiens (man)
 C:Date: 07-Feb-1992 #sequence_revision 26-May-1995 #text_change 17-Mar-2000
 R:Tsugu, H.; Horowitz, R.; Gibson, N.; Frank, M.B.
 Genomics 24, 541-548, 1994
 A:Title: The location of a disease-associated polymorphism and genomic structure of t
 A:Reference number: A37241; MUID:91086445; PMID:1985094
 A:Accession: A37241
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-475 <TSO>
 A:Cross-references: GB:013657
 R:Itoh, K.; Itoh, Y.; Frank, M.B.
 J. Clin. Invest. 87, 177-186, 1991
 A:Title: Protein heterogeneity in the human Ro/SSA ribonucleoproteins. The 52- and 60
 A:Reference number: A37241; MUID:91086480; PMID:1985112

A:Accession: A37240
A:Molecule type: mRNA
A:Residues: 1-51, A', 53-475 <CH>
A:Cross-references: GB:M62800; NID:g338489; PID:AAA36651.1; PID:g338490; GB:M35041
C:Gene: GDB:SSA1
A:Cross-references: GDB:133758; OMIM:109092
A:Map position: 11p15.5-11p15.5
A:Introns: 136/3; 168/3; 245/3; 253/2; 287/1
C:Superfamily: rfp transforming protein; RING finger homology
C:Keywords: DNA binding; nucleus; zinc finger
F:12-60/Domain: RING finger homology <RNG>
F:16-54/Region: zinc finger C3HC4 motif

Query Match 22.18; Score 552.5; DB 1; Length 475;
Best Local Similarity 31.38; Pred. No. 4.1e-27;
Matches 150; Conservative 88; Mismatches 208; Indels 33; Gaps 14;

QY 7 DELICSTICSTIYQDPVSLGCEHYFCRCITHEWYRQEQARDCPECHRTAEAPALAPSL 66
DB 12 EEVCPICLPDFEVPVSECHSFCQECISQ---VGGGGSVCPVCRORFLKLNLRNR 67
QY 67 KLANIVRYSSFPDLAILNARRAAPCOAH--DKYKLFCLTDRLALCFCDPEPALHEOHQV 125
DB 68 QLANVNNKKEISGA--RETOGERCAVHGERLHLCEKDGKALCWCAOSKRKHROHAM 125
QY 126 TGIDAFDELQRELKDLQALQALDSEHTEALQF--LKROLAETKSTKSLRTTIGRAF 182
DB 126 VPLEAAQEQYQKQVLAELR--RKQELAEKLEVEIAIKR--ADMKTVEYQKRIHAFF 182
QY 183 ERLHRLREROKAMLELEADTARTLDIEQKVORYSQOLAKVQBGAILDERLAETPRH 242
DB 183 VQGNFLVEEQROLOLEKDEREQLRIIGKEAKLAQO-----SOALQELISELDR 235
QY 243 TFLGAVASLSERL--KGIHETNLTYEDFPYSKYTGPLQYTIKMSLFOD--IHPVALYT 298
DB 236 CHSALFELQEVILVLEKSESWMKLDIDITSEPLRSVCHVGLKMLATCAVH-----IT 290
QY 299 LDPETAHORLILSDCTIVAYGNLHPOPLDSPRFDEVSVLGSSEASGVHWYEVVA 358
DB 291 LDPTTAPFWLISDRKQVRLGDTQ--QSIPTNERFESYPVAVLAQHHSKHWEDVYT 349
QY 359 EKTQWVGLAHEASRKGSIQIOPSRGYCIVMHDGNOYSCTEPMRLNRYDLKRGV 418
DB 350 GKEAMDAGVCRDSTRKRGHFLSKSGFWITWLNKKQKYEAGTIPQPLHLQVPPCQGI 409
QY 419 FLVDYQGLITFYN--ADMSWLYTFR--KEPGKLSYSPGOSHANGKVPRLINTVRI 475
DB 410 FLVDYQAGVSPYNTDHSGLTYSFSECAFETGPLRPFSPG--FNDGKMTATLTLCLPLNI 467

RESULT 7
JE0343
terf protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jun-2000
C:Accession: JE0343
R:Ogawa, S.; Goto, W.; Orlino, A.; Hosoi, T.; Ouchi, Y.; Muramatsu, M.; Inoue, S.
Biochem. Biophys. Res. Commun. 251, 515-519, 1998
A:Title: Molecular cloning of a novel RING finger-B box-collided coil (RBCC) protein, terf
A:Reference number: JE0343; MUID:99011410; PMID:9792805
A:Accession: JE0343
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <OGA>
C:Superfamily: rfp transforming protein; RING finger homology
F:12-71/Domain: RING finger homology <RRN>

Query Match 18.98; Score 472.5; DB 2; Length 477;
Best Local Similarity 28.98; Pred. No. 4e-22;
Matches 147; Conservative 81; Mismatches 203; Indels 77; Gaps 19;

QY 1 MACSLKELCLSTICSTIYQDPVSLGCEHYFCRCITHEWY-----RQEQARDCPEC 53

DB 6 LARRLOEATSTICIDYTTDPMACGHNFCRECIQMSKRGKRGKKGSPCEC 65
QY 54 RRTFAEPALASLKLANIVRYSSFPDLAILNARRAAPCOAH--DKYKLFCLTDRLALCF 112
DB 66 REMSPQRULRRNRLITKAEMARQHP---GLHKRL---CQIHQEPKLFCQDDQPTPCV 119
QY 113 FCDEPALHEOHQVGTIDAFDELQRELKDLQALQALDSEHTEALQILKRO--LAETKST 171
DB 120 VCREAQEHRMRVLPDLBAAREYKLRLEDIKYLE--EMMTETLQAEQDTLEWQERV 178
QY 172 KSLRTTAEAFERLRLREROKAMLEL---EADTARTLDIEQKVORYSQOLRKV--- 225
DB 179 KERRRILIEEQKVALFLVEEPEPLQLQIKKEEDTLQKQDSKASLDHQSRSLDLILQ 238
QY 226 -----QGAQILDERLAETDRHTFLAGVASISERLKGIHETNLTYEDFPYSKYT---G 276
DB 239 LEBOTQDEPLQMD-----VKDTLRKESLSHQFEVVL-----PVALKTYCRV 283
QY 277 PLQYTIKMSLRFODIHPVPALTLDPGTARHRLILSDCTIVAYGN-----LHPOPLDSP 331
DB 284 PGQLEVLKSFQEDVVP-----DSTAYPYLL-----YESRQRRLYSPPEGSAP 328
QY 332 ---KRPDEVSVLGSSEASGVHWYEV--VVAETQWVGLAHEASRKGSIQIOPSRGF 386
DB 329 YSKRFLAYPCAVQKSFSSGRHWEGMNLTDGALMALGYCRNVSKRDVFLKSPENG 388
QY 387 YCIWHDGQYSACTEPTRLNVRDKLDKGVFLDYDQGLIFYNADMSWLYTFR--KE 445
DB 389 WVVLQSKKRLPLPLNPIPTLTPRPSHMOIFLDFQAGEVSFTSYNDGSHLSFSQYAF 448
QY 446 PGKLSYSPGOSHANGKVPRLINTV 473
DB 449 GGLPLFEFCIG--SPKSGQMV-----ISTV 471

RESULT 8
T09482
ring finger protein fxy - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C:Accession: T09482
R:Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A:Description: The human fxy maps to chromosome Xp22.3: Implications for evolution of
A:Reference number: 216687
A:Accession: T09482
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PER>
A:Cross-references: EMBL:AF035360; NID:g2827993; PID:g2827994
C:Gene: fxy
C:Genetics:
A:Gene: fxy
A:Map position: Xp22.3
C:Superfamily: RING finger homology
F:6-65/Domain: RING finger homology <RRN>

Query Match 14.98; Score 372.5; DB 2; Length 667;
Best Local Similarity 21.68; Pred. No. 1.1e-15;
Matches 142; Conservative 93; Mismatches 199; Indels 223; Gaps 23;

QY 4 SLKDELICSTICSTIYQDPVSLGCEHYFCRC---ITHEWYRQEQARDCPECHRR- 55
DB 3 TLESELTCPLLEFEDPLLPCHASLFCNCAHRLVSHCATNSVESITAFQCPTRHV 62
QY 56 -TPAE--PALAPSLKLANIVRYSS-----SPDLAILNAR----- 87
DB 63 ITLSQRLDGLKRNVTIQLNIDFQKASVSGSPNSPSTRERRADANTMTSAEKVLCQFC 122
QY 88 -----RAAP-----COAH--DK 98
DB 123 DQDPAQAVKTCVCEVSYQDECLKATHPKKPTGTHRLIEPIPSHSIRGLMCLEHDEK 182

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QY 99 VKLUCITDRALLCFFCDEBPALHEQOYVIGIDDAPELORELKDOUAL--ODSEEHTEA 156
Db 183 VNMVCVTDDOJICALCKLVGRHROHQAALSERDYKLOMENSETNJNKRNETLETLLA 242
QY 157 LQILKROLAETSSSTKSLRTTIGEAFFERHRLREBORAKMELEPADTARTJTDIOEKVO 216
Db 243 KLITQCHVEVEMASROEAKLT--EBCDDLIIEIQORRQIIGIKKEGVMRLAKLAQQA 300
QY 217 RYSOOLKRVQGAQIIOERLAETDRHTFLAGVASISERL-----KGIHETNL--TYE 267
Db 301 NCKOCIEKSASLISOAEHSLKENDHARELOTAKNITEREVSMAATASSQVLEIPEININDEFD 360
QY 268 ---DEPRSK-----YTGp-----LOYTI 282
Db 361 TFAIDFSNEKLLIECDYLTAPNPPTEIBELCTASYDITIVHWISDDEFSVSYELOXTI 420
QY 283 -----W-----KSLFODIHPPVA----- 296
Db 421 FTGOANVSYLCSNDSWMIIVENIKONHYTHAIGLOSTKYIFWAKAINAGSSRSEPGKLL 480
QY 297 -----LTLPDCTAORULLSDDCITVAAGNHLPOGLDS-----PKRPDVEVS--YLGs 343
Db 481 TNSOPFKLDPWSAHKKLVASHD-----NLIVEDESSSKSSHPPERTSGSGVAGVAN 533
QY 344 EAFSSGVHVEVVAEKTQWVIGLHAHEAASRKGSIOIOPSRGYC-----TYMHGDNGQY 397
Db 534 VFIDSGRHYMEVVISGSTWVAIGLAKYSAPKHEWIGKMSASWALCRONNNWVVRHNSKRI 593
QY 398 SACTEPPWRLANVRDKLVGFPLDYDOGLLIFYNADDMSWLTTEPEKKPPGKICSTFS 454
Db 594 PIEPAPHLR-----RVGILLDDNDSIAFYDLNLSIHLYTFPVAAQOPVCPPTPT 642

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RESULT 9
T12494
hypothetical protein DKFZp34C091.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Sep-1999
C:Accession: T12494
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, June 1999
A:Reference number: 217525
A:Accession: T12494
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <P00>
A:Cross-references: EMBL:AL080170
A:Experimental source: adult testis; clone DKFZp34C091
C:Genetics:
A>Note: DKFZp34C091.1
C:Superfamily: rfp transforming protein; RING finger homology

Query Match      14.8%; Score 370.5; DB 2; Length 438;
Best Local Similarity 30.2%; Pred. No. 8.3e-16;
Matches 105; Conservative 56; Mismatches 140; Indels 47; Gaps 9

Db      126 TGIDDAFDELQRELKQDLQALQDSERHEALQILQILQ--AETKSTKSLPTTIGE-- 180
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
      80 SGALGADMLVAQVYLQW-----ALEIKRELELDALTEAVANGKRTVIMKEKV 127

QY      181 -----AFERHLRLREROKAMLELEADPTATLTDIEQKVORYSQQLKRVQDGAOI 231
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
      128 EMORQREFLEKHKHGFALQEOEQQLRLRLAEERATLQRLRKSRSLVQSSKALELDE 187

QY      232 LOERLAERDRATPLAGVASLSERLKGKIHENLTYLEDPTSKYNG---PLQYTIKSLFQ 288
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
      188 LQER-CQRPALGLLEGVAGVLSRSKA---VTRLEENIPMEIKTYACCTGPRRELLRKFOV 243

QY      289 DIHNPALATLPDPCGHAQRLILSDCCTIVAGCNLHROPLOD---SPKRIVDEVSYGSEA 345
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
      Db      244 DY-----KIDPATNPSLITLADLRKYODS---EPKRDVPPNPRFDTPYCTIGLOS 292

QY      346 FSSGHWYEVVAETQWVIGLAHBAASRKGSIQIOPSRKGFYCIWHDGNGNSACTEPT 405

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Db      293  FSSGHHYEWVLEGEAEWGLGVCODTLPRKGETMSPSPENGVMALMTLTKENYKMYLSPSY 3522
Oy      406  RLNVADKLDKRGVGFLLDYDQGLLIFYNADMSMLYTFRERFPGKLCYF 453
Db      353  PLQLESPRCIGIFLDYENGELSFYNVWDGSIYTFNQLSGLLRPF 400

RESULT 10
T09013
RING finger protein Fxy - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Sep-2000
C:Accession: T09013
R:Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A>Title: A gene spans the pseudautosomal boundary in mice.
A:Reference number: Z16531; MVID:98004518; PMID:9342357
A:Accession: T09013
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PAL>
C:Genetics:
A:Gene: Fxy
A:Map position: X; Y
C:Superfamily: RING finger homology
C:Keywords: zinc finger
E7-65/Domain: RING finger homology <RNR>

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Query Match	14.6%	Score 364.5	DB 2	Length 667
Best Local Similarity	21.8%	Pred. No. 3,4e-15		
Matches 143	Conservative	87	Mismatches 204	Indels 223
			Gaps	23
QY	4	SLKDELACISICLSITODPVSIGCEHYFCRC---	ITEMVRO---	EAGGARCPCCR- 55
DB	3	TLLESLTOPICLELEDPLLLPCASLSCNCARILYSHCATNEPEVSEINAFCCPFCRIY	62	
QY	56	-TPAE--PALAPSKLANIVERYS-----	SEPIDAILMAN-	87
DB	63	ITLSORGLDGLKRNVTLONIIDRFKASVSGNPSETRERAFDANTWSSAKRYLCOPC	1222	
QY	88	-----RAAR-----	COAH--DK	98
DB	123	DODPAQDAVKTCVCEVSYCDCECLKATPHNKKPFTFGRIIEPLPSHINGLTGLEHEDE	1822	
QY	99	VKLECLTDRALLCFCEDEPALHBOHQVYTGIDDAFELQRELKDOAL--	ODSERHTEA	156
DB	183	VMMCVTDQDQILCALCKLWGRHQRHVAALSERYDKLQNLBESLNFLNKRTELETLA	242	
QY	157	LQILKROLAETKSSRKSLRTTYTGEAFERHLLREKQKMBLELDVARTLTIDIOKYO	216	
DB	243	KLIOTQOHEVNAASQOEAKLT--ERCDDLIETIIIOQRQILGTIKIKGKVIIRLKLAAQOA	300	
QY	217	RYSQOLRVQOEGAQILOERLAEETDRHFTLAGVASLSERL-----	KGKIHETNL--TYE	267
DB	301	NCKQCLERSASALISQAHSLSKENDARFLQTAKNITERYSMATASSQVLLPEINLMDTD	360	
QY	268	---DEPTSK-----YTGp-----	LOYTI	282
DB	361	TFALDFSRKKLLECDLYLTAPNPAIREELCTASVDTITVHWTSEDEFSVSYELQYTI	420	
QY	283	-----W-----KSLFQDIHVPAA-----		296
DB	421	FTGQANVSLCNSADSMMILVPIKONHYTVHGLQSGTKYIFTYKAINQAGSRSSBEGKIK	480	
QY	297	-----LTLDPGFAHORLITLSDQCTIYAAGNLBPOLQDS-----	PKREFDERS--VLGS	343
DB	481	TNSQFRLDPKSAHRLKLVSHD-----NLIVERBESSKSKSHAPERFAGOSYGVAGN	533	
QY	344	EAFSSGVHWEVYVAEKTQWVIGLAHEAASRKGSIQIOPSRGYC-----	IYMHGANOY	397
DB	534	VFIDSGRIHWEVYVAGSTWYALGAYLRSPKRIHEMIKNNAASWMLCCHNHNAVAFHQKGE	593	

A:Accession: I49642
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-634 <RES>
 A:Cross-references: GB:D63902; NID:g1088466; PIDN:BAA09941.1; PID:g1088467
 C:Superfamily: RING finger homology
 C:Keywords: zinc
 F:9-59/Domain: RING finger homology <RNG>

Query Match 12.2%; Score 304.5; DB 2; Length 634;
 Best Local Similarity 19.8%; Pred. No. 1,7e-11;
 Matches 125; Conservative 99; Mismatches 210; Indels 197; Gaps 20;

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OY 5 LKDELCSICLSIYDQPVSLGCEHYECRCITENHWKQEAQG-ARDCEGRTE-APAL 62
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 7 LAELSCSYCLELFKEVVTTPCGHNCTSCLEDTWV---VQPPRCPCQCKRYQVAPQL 63
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 63 APSLKANIYER-----SSFPID-----ALNARRARP----- 92
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 QKNTVCAVVEQFLQAEQARTPVDDWTPPARFSASAAVACDHCITETAVKTCVMA 123
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 93 --CGAH-----DKVRLFCITDRALCFRDEP-----ALHE 121
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 SFCQELHRRFEDSPADHPLOSPIRDLLRKCTQHNRLKEPFCPEHCICHLVEHK 183
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 122 QHQVTGIDAFDELQBELKDQALQDSEREHTEALQLRLQALAEKTSKSLTGTGEA 181
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 184 TCSPTTILSQASADLEYKLRNKLITIMSHINGATRALE-----DVNSKQCCVQDSMKR 236
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 182 FEYHLHLREROKAMELEADARITLDEQVQ-----RYSQQLRKVQGAQ 230
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 237 MEGLRQRYME-MRAVIDAETSSLRLKEEKRYGKFDITVYLVKKSSEMOKLKAWE 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 231 ILQERLAETFRHFFL-----AGVASLSERLKGKI- 259
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 296 LINDK---GDEFFLEKAAALQGESEKPYIIPKIDLDHLMIGYGAADLKSELKHSIK 352
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 260 -----HETNLYEDPPTSKYT----- 275
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 353 KLOKKESEHNSGNKQGTQSTFKPVQPSKKTIOEKTKKTPVAPCPSPHSFKLPTFG 412
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 276 GPLOYITKSLFDIHVPAA-----LITDPSTAH 305
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 413 APQOSLDSKATSPDAAPKASAAOPDSIGVAKYLENLETKSRTELEYEVKVFEDYNTAH 472
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 306 QRLILSDDCITVAYGNLHPQLDSPKRFPEVSVLGESEAFSSGVHWYVVAEKQWVI 365
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 473 NKXSLSKYTTTASVD-GLOHTKSHPOKFTYCSQVLAGHCYKNGIHWEVELQKNFCGV 531
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 366 GLAHEASARKG-SIQIQPSRGFYCIYMHGNOYSACTEPWTRLNVRDKLDRGVFLDYDQ 424
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 532 GICYGSMERGSPSRIGRNPNMVCWEFN-NKISAMNNVETKLPSTKATRVGLVLCNDH 590
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 425 GLIIFYN-ADDMGMLTYFRKFKPGKLCYSF 453
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 591 GFVIFPAVTEKVMHMKFKVDFTFALYPAF 620
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 14

A37821
 butyrophillin - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
 C:Accession: A37821
 R:Jack, L.J.W.; Mather, I.H.
 J. Biol. Chem. 265, 14461-14466, 1990
 A:Title: Cloning and analysis of cDNA encoding bovine butyrophillin, an apical glycoprotein
 A:Reference number: A37821; MUID:90354441; PMID:2387867
 A:Accession: A37821
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-526 <JAC>

A:Cross-references: GB:M3551; NID:g1763685; PIDN:AAB39766.1; PID:g162773
 C:Keywords: transmembrane protein

Query Match 12.0%; Score 301.5; DB 2; Length 526;
 Best Local Similarity 41.3%; Pred. No. 2.1e-11;
 Matches 71; Conservative 24; Mismatches 70; Indels 7; Gaps 5;

```

OY 283 WKSLFDIHVPALTLDPGTAHQRLILSDCTIVAYGNLHPQLDSPKRFDEYEVVLG 342
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 295 WKR--ATLHAVD--VTLDPTAHPHLFLYEDSKSVRLSDSR-QKLPRKPRFDSWPCVMG 349
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 343 SEAFSSGVHWYEVVAEKTQWVIGLAHAASRKSGSIQPSRGFYCIYMHGNOYSACTE 402
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 350 REAFSTGRHWYEVVGGRTDMALGVCRENWKKGFDMTPENGFWAVELY-GNGYVALTP 408
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 403 PWRFLNVRDKLDRKGVFLDYDQGLIIFYNADDMGMLTYF--REKPGKLCYSF 453
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 409 LRTPLPLAGPPRRKGVFLDYESGDIIFYNMTDGSHTYFSKASPSGLRPF 460
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 15

S70587
 butyrophillin precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 R:Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Coueto, J.R.
 Biochim. Biophys. Acta 1306, 1-4, 1996
 A:Title: Cloning and sequence analysis of human butyrophillin reveals a potential recep
 A:Reference number: S70587; MUID:96201696; PMID:8611614
 A:Accession: S70587
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-526 <TAY>
 A:Cross-references: EMBL:U03576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083

Query Match 11.7%; Score 293; DB 2; Length 526;
 Best Local Similarity 25.6%; Pred. No. 7.2e-11;
 Matches 127; Conservative 71; Mismatches 195; Indels 104; Gaps 21;

```

OY 15 LSIYQDVSIGC-----EHYCRRCITENHWKRA-----QGANDCEC- 53
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 39 LAVGEDAELEPCRLSPNASEHLEL-----WPKKRVSPAVLVRDGRDEADQMPERYR 92
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 54 -RRFPAPALAP---SLKANI-----VERYSF-----PLDILNARRARPCQANDKV 99
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 93 GRATLVODGIAKGVALARIGVRSVDGEYTCFFREDGYSREALVHLKVALGSDPHISM 152
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 100 KLFCLTRALLCFECDEPALHEHQVYTGIDAFDELQRELKDQLQALQDSEREHTEALQL 159
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 153 Q--VOENGELCECTGVGWPERQY-----QWRTSGKEKFPSTSESNNPDEGLFT 201
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 160 LKROLAETKSKTKLRTTIGAEFRLRLEROKAMLELEADTARTLTDIEQVORYS 219
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 202 VAASVILRDTSTKNVSCI-----ONLLGQEKKEIISIPASSLRLPWIYAVAVIL 254
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 220 QQLKRVQEGA-----QILOERLAETDRHTPLAGVASISERLKGKIHETNLYEDPPTSKY 274
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 255 MVLGLITGTISTFTWRLYNERPRER-RNEF-----SSKERL----- 289
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 275 TGPLQYITKSLFDIHVPALTLDPGTAHQRLILSDCTIVAYGNLHPQLDSPKRF 334
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 290 ---LEELKWKK--ATLHAVD--VTLDPTAHPHLFLYEDSKSVRLSDSR-QKLEKTERF 341
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 335 DVEVSVLGEAFSSGVHWYEVVAEKTQWVIGLAHAASRKSGSIQPSRGFYCIYMHG 394
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 342 DSMFCVIGREFTTSGRHWYEVVGDRTDMAIGVCRENWKKGFDMTPENGFWAVELY-G 400
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 395 NOYSACREPMTRLNVRDKLDRKGVFLDYDQGLIIFYNADDMGMLTYFRE-KFPGKLCYSF 453
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 401 NGYVALPLPLPLPLAGPPRRKGVFLDYESGDIIFYNMTDGSHTYFSKASPSGLRPF 460
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 454 SPQSHANGKNVQPLRI 470
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

Db 461 CLMS---GK--KPLTI 472

Search completed: October 7, 2003, 17:51:24
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 17:38:26 ; Search time 25 Seconds
(without alignments)
893.507 Million cell updates/sec

Title: US-09-927-091-1
Perfect score: 2504
Sequence: 1 MACSLKDELLACISLISYOD.....GSHANGKNVOPLRINTVRI 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	772	30.8	624	1 A33_PLEWA	002084 pleurodeles
2	663.5	26.5	518	1 RN22_HUMAN	09hcm9 homo sapien
3	653.5	26.2	488	1 RN23_MOUSE	09esm2 mus musculu
4	583	23.3	513	1 RFP_HUMAN	P14373 homo sapien
5	580	22.2	522	1 RFP_MOUSE	062158 mus musculu
6	560	22.4	468	1 TM11_HUMAN	096f44 homo sapien
7	554.5	22.1	467	1 TM11_MOUSE	099p92 mus musculu
8	552.5	22.1	475	1 RO52_HUMAN	P19474 homo sapien
9	528	21.1	470	1 RO52_MOUSE	062191 mus musculu
10	505.5	20.2	488	1 TRM6_HUMAN	09c030 homo sapien
11	489	19.5	465	1 RN15_HUMAN	000635 homo sapien
12	456	18.2	489	1 RNFP_MOUSE	09ud66 mus musculu
13	449.5	18.0	482	1 RNFP_HUMAN	09ud66 homo sapien
14	449	17.9	539	1 Z173_HUMAN	012839 homo sapien
15	430	17.2	465	1 TM15_HUMAN	09c019 homo sapien
16	427.5	17.1	781	1 MEV_HUMAN	015533 mus musculu
17	410.5	16.4	496	1 TM30_MOUSE	P15533 mus musculu
18	372.5	14.9	667	1 MID1_HUMAN	015314 homo sapien
19	369.5	14.8	667	1 MID1_RAT	P82458 ratius norv
20	362	14.5	680	1 MID1_MOUSE	070583 mus musculu
21	360.5	14.4	667	1 MID1_MOUSE	P82458 mus musculu
22	341	13.6	630	1 Z147_HUMAN	014258 homo sapien
23	321.5	12.8	442	1 TM14_HUMAN	014142 homo sapien
24	306	12.2	288	1 RFL1_HUMAN	075677 mus musculu
25	304.5	12.2	634	1 Z147_MOUSE	P61550 mus musculu
26	301.5	12.0	526	1 BUTY_BOVIN	P18892 bos taurus
27	297.5	11.9	524	1 BUTY_HUMAN	062556 mus musculu
28	296	11.8	288	1 RFL2_HUMAN	075678 homo sapien
29	295	11.8	288	1 RFL3_HUMAN	013410 homo sapien
30	293	11.7	526	1 BUTY_HUMAN	09ns80 homo sapien
31	279.5	11.2	452	1 RN18_HUMAN	09bz29 homo sapien
32	276	11.0	425	1 TM31_HUMAN	09bz29 homo sapien
33	269	10.7	551	1 RN27_MOUSE	099p2 mus musculu

34	267	10.7	551	1 RN27_HUMAN	09bz29 homo sapien
35	263.5	10.5	407	1 RFP2_HUMAN	060858 homo sapien
36	248.5	9.9	353	1 RN28_HUMAN	096991 homo sapien
37	242	9.7	221	1 TRM2_HUMAN	09c029 homo sapien
38	224	8.9	744	1 TRM2_HUMAN	09c040 homo sapien
39	224	8.9	744	1 TRM2_MOUSE	09esm6 mus musculu
40	213	8.5	744	1 TRM3_HUMAN	095382 homo sapien
41	211	8.4	436	1 TRM3_HUMAN	09byy6 homo sapien
42	207	8.3	744	1 TRM3_MOUSE	09i12 mus musculu
43	207	8.3	744	1 TRM3_RAT	070277 ratius norv
44	158.5	6.3	653	1 HT2A_HUMAN	013049 homo sapien
45	155.5	6.2	974	1 YMB4_CAEEL	003601 caenorhabdi

ALIGNMENTS

RESULT 1
A33_PLEWA STANDARD; PRT; 624 AA.
ID 002084;
AC 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc-binding protein A33.
OS Pleurodeles waltl (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae;
OC Pleurodeles.
OX NCBI_TaxID=8319;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=93154311; PubMed=7679068;
RA Bellini M., Lacroix J.-C., Gall J.G.;
RT "A putative zinc-binding protein on lampbrush chromosome loops."
RL EMO J. 12:107-114(1993).
CC -!- FUNCTION: MAY BE A NUCLEAR REGULATORY PROTEIN THAT IS STORED
CC IN THE GERMAL VESICLE FOR USE DURING EARLY EMBRYOGENESIS
CC AND MAY PLAY A ROLE IN THE SYNTHESIS OR PROCESSING OF PRE-MRNA
CC DURING OOCYTESIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: IT FIRST APPEARS ON THE CHROMOSOME LOOPS
CC AND IN THE NUCLEOLUS OF THE GERMAL VESICLE (GV). IT IS
CC TRANSMITTED TO THE EGG AT GV BREAKDOWN AND APPEARS IN EMBRYONIC
CC NUCLEI AT THE MID-BLASTULA STAGE AND IS FOUND IN MANY BUT NOT
CC ALL NUCLEI AT STILL LATER STAGES OF EMBRYOGENESIS.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 B box-type zinc finger.
CC -!- SIMILARITY: Contains 1 SPRY domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L04190; AAA49614.1; -.
DR PIR; S28418; S28418.
DR InterPro: IPR001870; B302.
DR InterPro: IPR003649; Bbox_C.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY_Receptor.
DR InterPro: IPR000315; Zn_finger.
DR InterPro: IPR001841; Zn_finger.
DR Pfam; PF00622; SPRY_1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00093; zf-C3HC4; 1.
DR SMART; SM00502; BBox; 1.
DR SMART; SM00336; BBox; 1.
DR SMART; SM00589; PRY; 1.


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DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BOX; 1.
DR PROSITE; PS00118; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR ZINC-finger; Nuclear protein; Developmental protein; Colled coil;
KM RNA-binding.
FT DOMAIN 19 26 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT ZN_FING 134 149 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT ZN_FING 132 202 RING-TYPE.
FT ZN_FING 238 269 B BOX-TYPE.
FT DOMAIN 337 386 COILED COIL.
FT DOMAIN 449 619 SPRY.
SQ SEQUENCE 624 AA; 71056 MW; 60DBD1F3F071EFD CRC64;

Query Match 30.8%; Score 772; DB 1; Length 624;
Best Local Similarity 35.3%; Pred. No. 2e-38;
Matches 170; Conservative 81; Mismatches 194; Indels 36; Gaps 9;

OY 7 DELGSGISLTYQDPSVSGCEHYFCRCRTETEMVNOEGAGARDCECRRTFAPALAPSL 66
DB 158 EDLCPCLRSLEKEVYIECGHNFCKIDKSW---ESASAFSCPECKEVLTERKYYTNR 214
OY 67 KLANTVERYSSEPIIDAILNARRAPRQAND-KVYLFCULTRALCFECDEPALHBOHGV 125
DB 215 VLANLVKKAAYGVRKDKVPRK---EKCDHDERLTLFCDDGTCLACVICRDLKSNHNF 271
OY 126 TGIDDAFDELQRELKDOAL-----QDSEREHTALQLKROLAETKSTYSL 174
DB 272 LPIQDAVG---VYRDQILALVSPLETTMKNQKCKCOSOKISLHRENIYDCKKHIEC- 326
OY 175 RTTGAEFERLRLREKOKAMLELEADTARTLIDBOKVORYSQOLKVOEGAOIIOE 234
DB 327 -----EKKHLPKREKAKVEDLNAREGLKDMENLVKMTDNCETFEAISTQOS 380
OY 235 RLAEIDRHTFLAGVASLSERL-----KGIHETNLTYEDFPTSKYTGPLQYTIWKSLEPD 289
DB 381 RLNESDPIAFPLTIDISFKIECKCEHRKGVPAESVLYNNELSGRNPGLQIYIMKELNSV 440
OY 290 IHPVPAALTLDPGRANHOLILSDCTIYAGLHROPLODSFKRDEVSIVLGSFAFSG 349
DB 441 VQGLAPLTLDPNPAHMLVISEGLTSVKTDT-KQQLPDNPKRPSOCLILVYLGAGGFSG 499
OY 350 VHYEVVAERKTOWYIGLAHEAASRKSIOLOPSNGFCIYWHODNOSACETPEPTRLNV 409
DB 500 KHYEVEVGNKTANDVGNASSESNKKGKIKLPAKGYIAIMLRNNAKFALESFSTKTLNL 559
OY 410 RDKLDKVGVLIDYDQGLLIFYNADDMWLYTFEREKPGKLSYFSPGOSHANGKVNQPLR 469
DB 560 TSRSKISGVLYDEGGQVSYFNADMSPIYTFNGSFTEKLVPIYLSPIQD-SGKNAEPLK 618
OY 470 I 470
DB 619 L 619

```

RESULT 2

```

RN23_HUMAN STANDARD; PRT; 518 AA.
AC Q9HGM9; Q961B6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE RING finger protein 23 (Testis-abundant finger protein) (Tripartite
DE motif-containing protein 39).
GN TRIM39 OR RNF23 OR TRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;

```

```

RX MEDLINE=20462913; PubMed=11006080;
RA Orino A., Yamagishi T., Tomioka N., Yamauchi Y., Hishinuma T.,
RA Okada K., Suzuki M., Sato M., Nogi Y., Suzuki H., Inoue S.,
RA Yoshitaka K., Shimizu Y., Muramatsu M.;
RT "Molecular cloning of testis-abundant finger protein/ring finger
RT protein 23 (RNF23), a novel RING-B box-coiled coil-B30.2 protein on
RT the class I region of the human MDC."
RL Biochem. Biophys. Res. Commun. 276:45-51(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- ALTERNATIVE PRODUCTS;
CC Name=1;
CC IsoId-Q9HGM9-1; Sequence=Displayed;
CC Name=2;
CC IsoId-Q9HGM9-2; Sequence=VSP-005755;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: ubiquitous; highly expressed in testis.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
CC -1- SIMILARITY: Contains 1 SPRY domain.
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CC -----
DR EMBL; AB046381; BAB16374.1; -
DR EMBL; BC007661; AA070661.1; -
DR PIR; JC7387; JC7387.
DR HSP; P15919; IRND.
DR Gene; HGNC:10065; TRIM39.
DR MIM; 605700; -
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY.1.
DR Pfam; PF00643; ZF-B_box.1.
DR Pfam; PF00097; ZF-C3HC4.1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BOX; 1.
DR PROSITE; PS00118; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.

```

KW zinc-finger; Coiled coil; Alternative splicing.
 FT ZN_FING 29 70 RING-TYPE.
 FT ZN_FING 102 143 B BOX-TYPE.
 FT DOMAIN 181 250 COILED COIL (POTENTIAL).
 FT DOMAIN 390 515 SPRY.
 FT VARSPLIC 269 298 Missing (in isoform 2).
 FT VARSPLIC 269 298 /PIDD-VSP_005755.
 FT CONFLICT 137 137 P -> A (in REF. 2).
 SQ SEQUENCE 518 AA: 59716 MW: DA92B38F253B828 CRC64;
 Query Match 26.5%; Score 663.5; DB 1; Length 518;
 Best Local Similarity 32.8%; Pred. No. 3.8e-32;
 Matches 167; Conservative 85; Mismatches 196; Indels 61; Gaps 13;
 QY 4 SKDELICSTICSTIYODPVSLGCEHYFCRCRCITEHNVROEAGARD--CPECRRTFAEBA 61
 DB 22 NIQVASCVCLEYLEKEPIIECGHNFCACTIRMEDE----RDFPCVCKTSRYNS 77
 QY 62 LAPSLKIANIYERYSFPLDALINARRARPC-QAHDKVKLPCLTPDRALICFCDEPALH 120
 DB 78 LRPNROLGSMVE--IAKQLOAVKRIKIDSLCPQHHEALSLFCYEDQEAVALICAIASHH 135
 QY 121 EOHQVYGDIDAFDELORELKQLOALQDSEREHTEALQLKROLAETKSTSLRTTIGE 180
 DB 136 RHIVVPPDDATQOEYKEKLOKCLEPLEOKLOETTRCKSSEKKPGELKRVESRQQLIR 195
 QY 181 AFEHLRLRLEROKAMLEELADTARTLDIEOKVORYSOQL-----RK 224
 DB 196 EFEELHRLRDEQOVLRLSLEEE--ODILQRLRENAHIGDKRDLAHLAAVEYKGC 251
 QY 225 VQEGAOILQERLAELDRH---TFIAGVASLSER---LKGKHEHNLTYEDPPTSYTG- 276
 DB 232 LOSGEMKLDVSTLEKNIPRKFGSLSTICPRDHRLGLVKEIN-RECKVKTMEVTSV 310
 QY 277 -----PLOY-----TIWKSLEFODIHPVPAALTLDPGTAHQRLISDQCTIYAGN 321
 DB 311 STELEKNSNFPROFALRKILKQILADY-----TLDPETAHPMLVLSSEDKSKYVE 363
 QY 322 LHPQLODSPKRFDEVSVLGSSEAFSSGVHWEVVAEKTQWVTIGLAHEASRKSIOIQ 381
 DB 364 TRLRLDLPTRPRTFYPVLAETEGFTSGRHWEVEVGDRTIHNAVGVCRDSVSKGELPL 423
 QY 382 PERGVCIYMHGNOYSACTEPWTRLNVKIDKGVDFLDQGLILFNADMSKLYTF 441
 DB 424 PFTGWKRVKLMGDDYATATPTPTPLHIVKPKRKGIFLDYAGTLSEFYNVDRSHITYF 483
 QY 442 REKFPKLCISYFSGOSHANGKNOPLRI 470
 DB 484 TDTTEKIMPLFPFG-IRAGRKNAAPLTI 511
 RESULT 3
 RN23_MOUSE
 ID RN23_MOUSE STANDARD; PRT; 488 AA.
 OC Q9ESN2: 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 28-FEB-2003 (rel. 41, Last annotation update)
 DE RING finger protein 23 (Testis-abundant finger protein) (Tripartite
 motif-containing protein 39).
 GN TRIM39 OR RNF23 OR TRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE-20462913; PubMed-11006080;
 RA Orino A., Yamagishi T., Tomioka N., Yamauchi Y., Hishinuma T.,
 RA Okada K., Suzuki M., Sato M., Nogi Y., Suzuki H., Inoue S.,
 RA Yoshimura K., Shimizu Y., Muramatsu M.;
 RT "Molecular cloning of testis-abundant finger protein/ring finger

RT protein 23 (RN23), a novel RING-B box-coiled coil-B30.2 protein on
 the class I region of the human MHC.";
 RL Biochem. Biophys. Res. Commun. 276:45-51(2000).
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
 CC -1- SIMILARITY: Contains 1 SPRY domain.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB046382; BAB16375.1; -
 CC HSSP; P15919; 1RMD.
 DR MGD; MGI:1890659; Trlm39.
 DR InterPro; IPR001870; B302.
 DR InterPro; IPR006574; PRY.
 DR InterPro; IPR003877; SPRY_receptor.
 DR InterPro; IPR000315; Znf_Box.
 DR InterPro; IPR001841; Znf_Ring.
 DR Pfam; PF00622; SPRY; 1.
 DR Pfam; PF00643; Zf-B_Box; 1.
 DR Pfam; PF00097; Zf-C3HC4; 1.
 DR SMART; SM00336; BBOX; 1.
 DR SMART; SM00589; PRY; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS50119; ZF_BB0X; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW zinc-finger; Coiled coil.
 FT ZN_FING 29 70 RING-TYPE.
 FT ZN_FING 102 143 B BOX-TYPE.
 FT DOMAIN 181 250 COILED COIL (POTENTIAL).
 FT DOMAIN 390 515 SPRY.
 SQ SEQUENCE 488 AA: 56369 MW: 8CEC3E584541F9A2 CRC64;
 Query Match 26.2%; Score 655.5; DB 1; Length 488;
 Best Local Similarity 33.2%; Pred. No. 1e-31;
 Matches 165; Conservative 79; Mismatches 186; Indels 67; Gaps 12;
 QY 4 SKDELICSTICSTIYODPVSLGCEHYFCRCRCITEHNVROEAGARD--CPECRRTFAEBA 61
 DB 22 NIQVASCVCLEYLEKEPIIECGHNFCACTIRMEDE----RDFPCVCKTSRYNS 77
 QY 62 LAPSLKIANIYERYSFPLDALINARRARPC-QAHDKVKLPCLTPDRALICFCDEPALH 120
 DB 78 LRPNROLGSMVE--IAKQLOAVKRIKIDSLCPQHHEALSLFCYEDQEAVALICAIASHH 135
 QY 121 EOHQVYGDIDAFDELORELKQLOALQDSEREHTEALQLKROLAETKSTSLRTTIGE 180
 DB 136 RHIVVPPDDATQOEYKEKLOKCLEPLEOKLOETTRCKSSEKKPGELKRVESRQQLIR 195
 QY 181 AFEHLRLRLEROKAMLEELADTARTLDIEOKVORYSOQLRKVOEGAOILQERLAEND 240
 DB 196 EFEELHRLRDEQOVLRLSLEEE--EDDI-----LQRLRENAHIGDKRDLAHLAAVEYKGC 251
 QY 241 RHITLAGVASLSERLKGK-----IHETNLTLYEDPPTSKYNG-----P 277
 DB 240 -----LAHLAAVEYKGCLOSGFEMLKQVSKSTLECKEYKTPMEVTSVSELEKNSNP 292
 QY 278 IQY-----TIWKSLEFODIHPVPAALTLDPGTAHQRLISDQCTIYAGNHPQLODSPK 333
 DB 293 RQYFALRKILKQILADY-----TLDPETAHPMLVLSSEDKSKYVEVETRLDLPDTPOR 345
 QY 334 PVEVSVLGSSEAFSSGVHWEVVAEKTQWVTIGLAHEASRKSIOIOPSRGVCIYVMD 393
 DB 346 FTTFYPCVLAETEGFTSGRHWEVEVGDRTIHNAVGVCRDSVSKGELPLPLETGTWKRRLMN 405
 QY 394 GNOYSACTEPWTRLNVKIDKGVDFLDQGLILFNADMSKLYTFPREKFPKLCISYF 453

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DB 406 GDRKAAATTTPTPLHIVKPKRVGILFDYAGLSTFNVDNRSHITFTDTEKMPLE 465
QY 454 SPQSHANGKNVOPLR1 470
DB 466 YPG-IRAGRKNAAPLTI 481

RESULT 4
RFP_HUMAN STANDARD; PRT; 513 AA.
AC P14373;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zinc-finger protein RFP (Ret finger protein) (Tripartite motif protein
DE 27).
GN RFP OR TRIM27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88246464; PubMed=3380101;
RA Takahashi M., Inaguma Y., Hiai H., Hirose F.;
RT "Developmentally regulated expression of a human 'finger'-containing
RT gene encoded by the 5' half of the ret transforming gene.";
RT Mol. Cell. Biol. 8:1853-1856(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231161; PubMed=11331580;
RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,
RA Riganelli D., Zanatta E., Messali S., Cainera S., Guiffanti A.,
RA Minucci S., Pellicci P.G., Ballabio A.;
RT "The tripartite motif family identifies cell compartments.";
RT EMBO J. 20:2140-2151(2001).
CC -1- FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- DISEASE: RECOMBINATION OF THE N-TERMINAL OF RFP WITH A PROTEIN
CC TYROSINE KINASE PRODUCES THE RET TRANSFORMING PROTEIN.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
CC -1- SIMILARITY: Contains 1 SPRY domain.
CC -----
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CC -----
DR EMBL: J03407; AAA36564.1;
DR EMBL: AF230393; AAG50172.1;
DR PIR: A28101; TVHURF.
DR Genew: HGNC:9975; RFP.
DR MIM: 602165;
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:0005624; C: membrane fraction; TAS.
DR GO: GO:0004714; F: transmembrane receptor protein tyrosine kin. . .; TAS.
DR GO: GO:0008283; P: cell proliferation; TAS.
DR GO: GO:0007048; P: oncogenesis; TAS.
DR GO: GO:0007283; P: spermatogenesis; TAS.
DR InterPro: IPR001870; B302.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR000315; znf_Box.
DR InterPro: IPR001841; znf_fing.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; zf-B_Box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR PRINTS: PR01406; BBOXZNFINGER.

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DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; zf_BBOX; 1.
DR PROSITE; PS00518; zf_RING_1; 1.
DR PROSITE; PS00089; zf_RING_2; 1.
KW Proto-oncogene; Zinc-finger; Metal-binding; Chromosomal translocation;
KW Nuclear protein; DNA-binding.
FT SITE 315 316
FT FT BREAKPOINT FOR TRANSLOCATION TO FORM THE
FT FT RFP-RET ONCOGENE.
FT ZN_FING 16 57 RING-TYPE.
FT ZN_FING 96 127 B_BOX-TYPE.
FT DOMAIN 368 493 SPRY.
SO SEQUENCE 513 AA; 58489 MW; 6F963D9048D8A731 CRC64;

Query Match 23.3%; Score 583; DB 1; Length 513;
Best Local Similarity 29.1%; Pred. No. 2,1e-27;
Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;

5 LKDELCSICLSIYQDPVSLGCEHYFCRCITHEWVROEAGARDCPCRRTPAEPALAP 64
10 LQGETCPVCLQYFAEPMLDGNHICACGLARCGTAEIVNS--CPGCRFTFPQRIHNR 67
65 SLKANIYERYSPPLDAIILARRARP-----COAH-DKYKFLCTDRALLCFPC 114
68 NRHLANVQ-----LVQLRTERPSPGCGEYCEKREPLIKLCEEDOMPICVVC 118
115 DEPALHEQHYGTIDDAFDELRELKDOLALDSEERHTEALDLKRQ-----LAE 166
119 DRSREHRGHSVLPLEAVEGKEQIQNL-----DHLKRVADLKRRAAGEQARAE 170
167 TKSSTKSLRTTIGAEFERLARLR--RQAMLEEL-----ADTA 205
171 LLSTQMERKIVWEFQYLSLKEHEYRLARLEIDLALVNSINGAITQSCNISILS 230
206 RTLDIDIEKQVRYOQLKQVDEGMAQIIOERLAIEDR-----HTFLAGV 248
231 SLIQLEKQKQDPREL-----LQDIDTLISREKRIIPRPWTTPDQLERHIFAQKC 284
249 ASLSERLKGKTHETNLFEDEPTSKYGTPLQYTIWKSLSFDIHV---PALTLDPGTAA 305
285 LFTVESLK-----QFTKMSDMEK--IQELREQLYSVVTIDDPDAY 326
306 QRLISDDCTIVAYGNLHPQLQDSPKRFDEVSVALGSEAFSSGVYWEVVAEKTOVI 365
327 PSLILSDLRQVRSYLD-QDLPNPERFNLPCVIGSPCFIAGHHYWEVGDKAKWTI 385
366 GLAHEAMSRKSIQIOPSRGYCYIMHDGNGYSACTEPTWTLNVRDKDKGVFLDYDG 425
386 GVCEDSVCKRGKGVTSAPQNGFMAVSLWYKGKRYMALTSPTALPLRTPLQVRGIFLDYDAG 445
426 LLIFYNADMSMLYTF--REKFPGRKCSYFSGQSHANGKNVOPLR1 470
446 EVSYFVNTYERCHTFTFSHTATFCGVPRYFS--LTSGSKNAAPLTI 489

RESULT 5
RFP_MOUSE STANDARD; PRT; 522 AA.
AC O62158;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zinc-finger protein RFP (Ret finger protein) (Tripartite motif protein
DE 27).
GN RFP OR TRIM27.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-C57BL/6;
RA MEDLINE-97176437; PubMed-9023983;
RX Cao T., Shannon M., Handel M.A., Eckin L.D.;
RT "Mouse ret finger protein (rfp) proto-oncogene is expressed at
RT specific stages of mouse spermatogenesis.";
RL Dev. Genet. 19:309-320(1996).
CC -1- FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
CC -1- SIMILARITY: Contains 1 SPRY domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; LA6855; AA05354.1; .
DR MGJ; MGJ:97904; Trm27.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; Znf_Box.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Fing.
DR Pfam; PF006622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; SPRY; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR ZINC-FINGER; Metal-binding; Nuclear protein; DNA-binding.
FT ZN_FING; 25 66 RING-TYPE.
FT ZN_FING; 105 136 B_BOX-TYPE.
FT DOMAIN; 377 502 SPRY.
SQ SEQUENCE 522 AA; 59550 MW; BFD418DBA13340B7 CRC64;

Query Match 23.2%; Score 580; DB 1; Length 522;
Best local Similarity 28.7%; Pred. No. 3,2e-27;
Matches 149; Conservative 88; Mismatches 189; Indels 94; Gaps 14;

QY 5 LKDELICSTCLSTIYQDPVSLGCEHYFCRCRCITEHWVWROEAQARDCECRRTAEAPALAP 64
DB 19 LQDETCPCVCLQYFEPMMIDCGHNICACIARCMGALEFNVS--CPQCHETFPQRMARP 76
QY 65 SLKLANIVERYSFPLDAILNARRARP-----COAH-DKVIKFLCTDLRALCFPC 114
DB 77 NKLHNAVTO-----LKKQLRTERPSGPGGEMGVCEKHKRRLKYCDMDPJCVC 127
QY 115 DEPALEHOQVGTGIDAFDELQRLKQALQDSEHEFEALQLKRC-----LAE 166
DB 128 DRSREHRDHSVPLLEAVEGFEKQIQNRL-----DHLRVKDKLKRRAQEGARAE 179
QY 167 TYSSTSLRTTIGAEFERHLRLREKOKAMLELEADTAFTLDIEQVORYS----- 219
DB 180 LSLTQMERKIKYMEFEOLYHSIKREHYRLARLEELDIAVNSINGAIQFSCNTSHLS 239
QY 220 -----QGLRKVGGAQILQERLAETDR-----HTFLAGVASLSER 254
DB 240 GLIAQLEEKQOQPTRELDDIGTLISRAERIRIPEPWITPPDQEKIHIAQRCLEFTES 299
QY 255 LKRIHETNLTVEDEPFSKYTGPLQYTIWKSLEFQDHPV--PALTLDPGTAHORLIIS 311
DB 300 LK-----QTEKMQSDMER--IQELREAQLYSDVTLDPDTATPISLIIS 341

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QY 312 DDCITVAYGTLHQPLODSEKREDVEYVIGSEAFSSGVIHYWEVYAEKTOWYIGLAHEA 371
DB 342 DNLROYVSYLQ--ODLPDNDPERNLFPCCVIGSGPCFIFGRHYWEVVGDKAKMTIGVCEDS 400
QY 372 ASRKGSIQIQPSRGFCIVWHDNGVYSAQCEPMTRLNVRKLDKGVGLFDGGLIFVY 431
DB 401 VCRKGGVTSAPQNGFMAVNSLWYGEKWTALSPMTALPLRLDVRGVGLFDAGEVSFYN 460
QY 432 ADDMSWLTYF-REKFPGLCSYFSPQSGSHANGKNVOPLRI 470
DB 461 VTERCHFTFTHATFCQVPVRPYS--LSYSGGSARPLII 498

RESULT 6
TM11_HUMAN
ID TM11_HUMAN STANDARD; PRT; 468 AA.
AC 096F4; 09C022;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tripartite motif protein 11 (B1A1 protein).
GN TRIM11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RL Piecha D., Petersohn D., Ecks B., Krieg T.;
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 225-468 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE-22388257; PubMed-12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Feyh J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 395-468 FROM N.A.
RX MEDLINE-21231161; PubMed-11331580;
RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Iuzi L.,
RA Ragnaeili D., Zanaria E., Messali S., Calanca S., Giffanti A.,
RA Minucci S., Pelicci P.G., Ballabio A.;
RT "The tripartite motif family identifies cell compartments.";
RL EMO J. 20:2140-2151(2001).
CC -1- SUBUNIT: Binds cytoplasmic tail of Integrin alpha-1.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
CC -1- SIMILARITY: Contains 1 SPRY domain.
CC -----
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CC -----

DR EMBL; AF347056; AAM63957.1; -

DR EMBL; BC011629; AAI11629.1; ALT_INIT.

DR EMBL; AF220125; AAG53498.1; -

DR Genew; HGNC:16281; TRIM11.

DR InterPro; IPR001870; B302.

DR InterPro; IPR006574; PRY.

DR InterPro; IPR003877; SPRY_receptor.

DR InterPro; IPR000315; Znf_Box.

DR InterPro; IPR001841; Znf_Box.

DR Pfam; PF00622; SPRY. 2.

DR Pfam; PF00643; Zf_Box; 1.

DR Pfam; PF00097; Zf_C3HC4; 1.

DR SMART; SM00336; BBOX; 1.

DR SMART; SM00589; PRY; 1.

DR SMART; SM00184; RING; 1.

DR SMART; SM00449; SPRY; 1.

DR PROSITE; PS00119; ZF_BOX; 1.

DR PROSITE; PS00518; ZF_RING_1; 1.

DR PROSITE; PS00089; ZF_RING_2; 1.

DR Zinc-finger; Coiled coil.

FT ZN_FING 16 57 RING-TYPE.

FT DOMAIN 129 208 B_BOX-TYPE.

FT DOMAIN 339 458 COILED COIL (POTENTIAL).

FT CONFLICT 395 398 SPRY.

FT CONFLICT 467 467 APLR -> GSIP (IN REF. 3).

FT CONFLICT 467 467 P -> A (IN REF. 3).

SEQUENCE 468 AA; 52774 MW; 8DE4BDF79F221739 CnC64;

Query Match 22.4%; Score 560; DB 1; Length 468;

Best Local Similarity 32.5%; Pred. No. 4.2e-26;

Matches 154; Conservative 75; Mismatches 191; Indels 54; Gaps 16;

QY 1 MACSKDELICSLCISTYQDVSLGCEHYFCRCITTEHWQEOAGADCEPCRTFAEP 60

DB 6 LSTNJOEATCAICIDFTDPMVMDCGHNFRCIRRCWGCP--GPVACPCRELSAOR 63

QY 61 ALADSLKANIYVERSSPFLDAIINARRARP-----COAH-DKYVLFCLTRALICF 112

DB 64 NLRNRPPLAKKAE-----ARLHPSPVPQGVCAHREPLLAFCGDELRLCA 112

QY 113 FCDEPALHEQVYIGDAPFDELQRELKQALQADLSREHTEALQILKROLAET---K 168

DB 113 ACESGEMAHVRVPLDAAEDDLAKLEKSLHL---RKQMDALLFOAQADECVLMO 168

QY 169 SSTRSLRTTIGAEFERLRLREROKAMLELEADTARTLTLDIQKQVRSQOLRKVOEG 228

DB 169 KAVESQONVYGEFERLRRLAEBOQLQRLLEELEVLRLRNGAHLQO----- 221

QY 229 AOILQERLAETDRFTFLAGVASLSERLKG---KIHETNLYEEDPPTSKYTGFLAY-TIMK 284

DB 222 SAHLAELIALEEGCOLPALGLLOD-IKDALRVQDVLOPPE-----VPMELRTYCR 274

QY 285 --SLFODIHVPALVLTDPGTAGHRLIISDCTIVANGNLHPOLQDSKPRFDEVSVLG 342

DB 275 VPGIVETLRFRGQVLTDPDTANPELILSEDRRSVQRDLR-QALPDRPERFDPCVYLG 333

QY 343 SEAVSSGVHWYEVYAAKTOVIGLAHAASRKSGIOQPRGFYCIYMHGNOYSACTE 402

DB 334 QERTSGHWEVGVGRTSWALGVCRNVNRKKEGELSAAGFWILVFL-GSYNNSER 392

QY 403 PWTLRADKLKDGKGVFLDYDOGLLIFYNADMSMLYTFRE-KFPGKLCISYFSP 455

DB 393 ALAPL--RDPFRRGIFLDYAGHLSTYSATDGLTFIPFIPISGTLRPLFSP 444

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

DE Tripartite motif protein TRIM11.

GN TRIM11.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP [1]

RA MEDLINE-21231161; PubMed-11331580;

RA Raymond A., Meroni G., Pantozzi A., Merla G., Cairo S., Luzi L.,

RA Riganelli D., Zanaria E., Messali S., Calanca S., Guffanti A.,

RA Minucci S., Pelicci P.G., Ballabio A.;

RT "The tripartite motif family identifies cell compartments.";

RL EMBO J. 20:2140-2151(2001).

CC -1- SIMILARITY: Contains 1 RING-type zinc finger.

CC -1- SIMILARITY: Contains 1 B box-type zinc finger.

CC -1- SIMILARITY: Contains 1 SPRY domain.

CC -----

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CC -----

DR EMBL; AF220124; AAG53497.1; -

DR HSSP; P15919; 1RMD

DR MGD; MGI:213735; Trtm11.

DR GO; GO:0005737; Cytoplasm; IDA.

DR GO; GO:0005634; Cnucleus; IDA.

DR InterPro; IPR001870; B302.

DR InterPro; IPR006574; PRY.

DR InterPro; IPR003877; SPRY_receptor.

DR InterPro; IPR000315; Znf_Box.

DR InterPro; IPR001841; Znf_Ring.

DR Pfam; PF00622; SPRY; 1.

DR Pfam; PF00643; Zf_Box; 1.

DR Pfam; PF00097; Zf_C3HC4; 1.

DR SMART; SM00336; BBOX; 1.

DR SMART; SM00589; PRY; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS00449; SPRY; 1.

DR PROSITE; PS00119; ZF_BOX; 1.

DR PROSITE; PS00518; ZF_RING_1; 1.

DR PROSITE; PS00089; ZF_RING_2; 1.

DR Zinc-finger; Coiled coil.

FT ZN_FING 16 57 RING-TYPE.

FT ZN_FING 87 127 B_BOX-TYPE.

FT DOMAIN 128 207 COILED COIL (POTENTIAL).

FT DOMAIN 338 457 SPRY.

SEQUENCE 467 AA; 52579 MW; 82B7CF68807E9DAB CnC64;

Query Match 22.1%; Score 554.5; DB 1; Length 467;

Best Local Similarity 32.8%; Pred. No. 8.7e-26;

Matches 155; Conservative 75; Mismatches 190; Indels 53; Gaps 16;

QY 1 MACSKDELICSLCISTYQDVSLGCEHYFCRCITTEHWQEOAGADCEPCRTFAEP 60

DB 6 LSTNJOEATCAICIDFTDPMVMDCGHNFRCIRRCWGCP--GPVACPCRELSAOR 63

QY 61 ALADSLKANIYVERSSPFLDAIINARRARP-----COAH-DKYVLFCLTRALICF 112

DB 64 NLRNRPPLAKKAE-----ARLHPSPVPQGVCAHREPLLAFCGDELRLCA 112

QY 113 FCDEPALHEQVYIGDAPFDELQRELKQALQADLSREHTEALQILKROLAET---K 168

DB 113 IC-ESEHWHTVRVPLDAAEDDLKRLKSLHL---RKQMDAMLFQAAETCALMO 167

QY 169 SSTRSLRTTIGAEFERLRLREROKAMLELEADTARTLTLDIQKQVRSQOLRKVOEG 228

Db 168 KVESGRQNVLGEFELRLRLAEEOQLQKLEEELEVLPLRLREGAARLGGQSTQ----- 223
 QY 229 AQLIQLAEETDRHFLAGVASISERLKGRIHETNTLYDE---PTSKYTGPLQYTIWK- 284
 Db 224 ---LALISLESESRCLPALGLLD-----IKDALCRVDKVLQPPAVPMELR-IVCRV 274
 QY 285 -SLFQIHVVPALPTDPTGARHRLISDCTIVANGNLHPQLQSPKRFVDVYVLS 343
 Db 275 PGLVETLRFRDITLDPTANDELVLSDRSVQGE-QRQALPDPNPERFDGPGCVLGQ 333
 QY 344 EAFSSGVHWYVVAEKTOVMIGLAHEAASRGSIQPSRGYCIYMDGNQYSACTEP 403
 Db 334 ERTSRHRTWEVGVGQTSALGCVCKETANRKRKKGELSGNGWIIIVFL-GSFYNSNEPA 392
 QY 404 WTRLNVRDLRKVGLDYDQGLILFYNDMSWLYTFREK-FPGKLCYSFSP 455
 Db 393 FSPL--RDPKRVGIFLDYEAGHSFYSATDGLIFPTLETLSGTLRLPLFSP 443
 RESULT 8
 RO52_HUMAN STANDARD; PRT; 475 AA.
 ID P19474; O96RF8;
 AC 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 52 kDa Ro protein (Sjogren syndrome type A antigen) (SS-A) (Ro(SS-A))
 DE (52 kDa ribonucleoprotein autoantigen Ro/SS-A).
 GN SSA1 OR RO52.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP TISSUE=Thymocytes;
 RC MEDLINE=9108645; PubMed=1985094;
 RA Itoh K., Itoh Y., Frank M.B.;
 RT "Protein heterogeneity in the human Ro/SSA ribonucleoproteins. The
 RT 52- and 60-kD Ro/SSA autoantigens are encoded by separate genes.";
 RL J. Clin. Invest. 87:177-186(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT ALA-52.
 RX MEDLINE=91086480; PubMed=1985112;
 RA Chan E.K., Hamel J.C., Buyn J.P., Tan E.M.;
 RT "Molecular definition and sequence motifs of the 52-kD component of
 RT human SS-A/Ro autoantigen.";
 RL J. Clin. Invest. 87:68-76(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95229155; PubMed=7713506;
 RA Tsugu H., Horowitz R., Gibson N., Frank M.B.;
 RT "The location of a disease-associated polymorphism and genomic
 RT structure of the human 52-kDa Ro/SSA locus (SSA1).";
 RL Genomics 24:541-548(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96215393; PubMed=8625517;
 RA Keech C.L., Gordon T.P., McCluskey J.;
 RT "Structural differences between the human and mouse 52-kD Ro
 RT autoantigens associated with poorly conserved autoantibody activity
 RT across species.";
 RL Clin. Exp. Immunol. 104:255-263(1996).
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-96.
 RX MEDLINE=99134294; PubMed=9933563;
 RA Bepler G., O'Brian K.C., Kim Y.-C., Schneider G., Pitterle D.M.;
 RT "A 1.4-Mb high-resolution physical map and contig of chromosome
 RT segment 11p15.5 and genes in the LOH11a metastasis suppressor
 RT region.";
 RL Genomics 55:164-175(1999).
 RN [6]
 RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow R.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussdl T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.V., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Ribonucleoprotein particle composed of a single
 CC polypeptide and one of four small RNA molecules. It is present in
 CC all mammalian cells studied but has no known function. At least
 CC two isoforms are present in nucleated and red blood cells, and
 CC tissue specific differences in Ro/SSA proteins have been
 CC identified. The common feature of these proteins is their ability
 CC to bind HY RNAs.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus or
 CC primary Sjogren's syndrome often contain antibodies that react
 CC with normal cellular Ro protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
 CC -1- SIMILARITY: Contains 1 SPRY domain.
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 CC -----
 DR EMBL: U01882; AAB87094.1; -;
 DR EMBL: M34551; AAA36581.1; -;
 DR EMBL: M62800; AAA36651.1; -;
 DR EMBL: U13658; AAA79867.1; -;
 DR EMBL: U13657; AAA79867.1; JOINED.
 DR EMBL: AF391283; AAK76432.1; -;
 DR EMBL: BC010861; AAH10861.1; -;
 DR PIR: A55642; A37241.
 DR Genew; HGNC:11312; SSA1.
 DR MIM: 109092; -;
 DR GO: GO:0003677; F:DNA binding activity; TAS.
 DR GO: GO:0003733; F:ribonucleoprotein; TAS.
 DR GO: GO:0009405; P:pathogenesis; TAS.
 DR InterPro: IPR001870; B302.
 DR InterPro: IPR006574; PRY.
 DR InterPro: IPR003877; SPRY_receptor.
 DR InterPro: IPR000315; ZnF_Box.
 DR InterPro: IPR001841; ZnF_Ring.
 DR Pfam: PF00622; SPRY; 1.
 DR Pfam: PF00643; ZfR_Box; 1.
 DR Pfam: PF00097; Zf-C3HC4; 1.
 DR PRINTS; SM01406; BBOX2FINGER.
 DR SMART; SM00336; BBOX; 1.
 DR SMART; SM00589; PRY; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS50119; ZF_Box; 1.
 DR PROSITE; PS00518; ZF_Ring; 1.

DR PROSITE: PS50089: ZF_RING_2; 1.
 KM Systemic lupus erythematosus; Zinc-finger; Antigen; RNA-binding;
 KN Ribonucleoprotein; DNA-binding; Polymorphism.
 FT ZN_RING 16 55
 FT ZN_RING 92 123 B BOX-TYPE.
 FT DOMAIN 211 232 LEUCINE-ZIPPER.
 FT VARIANT 52 52 /FTID-VAR_013749.
 FT VARIANT 96 96 G-> R (IN dBSNP:2975162).
 FT VARIANT 231 231 /FTID-VAR_013750.
 FT VARIANT 231 231 E-> K (IN dBSNP:2554934).
 FT VARIANT 231 231 /FTID-VAR_013751.
 FT VARIANT 231 231 DDEF2944AFC629FB CRC64;
 SQ SEQUENCE 475 AA: 54169 MW: DDEF2944AFC629FB CRC64;
 Query Match 22.1%; Score 552.5; DB 1; Length 475;
 Best Local Similarity 31.3%; Pred. No. 1.2e-25;
 Matches 150; Conservative 88; Mismatches 208; Indels 33; Gaps 14;

OY 7 DELGCTSLSTYODVSGCEHYFCRCITTEHWVQEOAGARDCECRRTFAEPALASL 66
 DB 12 EEVTCIPCLDPVEVSVSIECGHCFCEKISQ---VGKGGSGVCPVCRORFLKMLRPNR 67
 OY 67 KLANIVERYSFPLDAILNARRAAP--COAH-DKVKLFCLTDRLALCFCEDEPALHEOHV 125
 DB 68 OLANNVNLKKEISGEA--REGTQGERCAVHGERLHLFECKGKALCWCAQSKRIHDIAH 125
 OY 126 TGIDDAFDELQRELKQALQALDSEHRETEALQ--LKROLAETKSTKSLRTTIGFAF 182
 DB 126 VPLEEAAQEQEKQLQVALGELR-RKQELAEKLEVEIAIKR--ADMKKTVEQKSRTHAEF 182
 OY 183 ERLHRLEROKAMLEELADTARTLDIEOKVQRYSOGLKRYOGAGLIIOERLAETRH 242
 DB 183 VQAKNLFVEERQROLQLEKDERQRLGLEKEALAQ-----SALDELSELDNR 235
 OY 243 TFLAGVASLSRL--KGIHETNLTYEEDPTSKYTGPLQYTIWKSLEFD--IHPYPAAL 298
 DB 246 CHSALDELQEVITYLESESMNLKDLDTSPELRSVCHVGLKMLTCAVH-----IT 290
 OY 299 LDPTGAHORLLSDCTIVAYGNLHPROLQSPKRFDEVEVYLGEAFSSGVHWEEVVA 358
 DB 291 LDPTGANFWLLISDRQVRLGDTQ-OSIPGNEERFDYPRVYLGQNHSGHWEVNVVT 349
 OY 359 EKTQWVIGLAHEAASRKSGIOIPSRGYCIAMHNGNOYSACTEHWTLNVRDKDXGV 418
 DB 350 GKEAMDAGVCDYRRKRGHFLISSSGFWTILNKKQYEGATTYQPTLHLQVPPCQVGI 409
 OY 419 FLVDYQGLLIFYN-ADDMSWLYTFRE-KFPGKLSYFSPGQSHANGKVVQPLRIINTVRI 475
 DB 410 FLDYEAGWVSFYNTIDHGLSLYSFSECAFETGPLRREFSPG-FNDGKNTAPLTLCLPLNI 467

RESULT 9
 ROS2_MOUSE STANDARD: PRT: 470 AA.
 AC Q62191.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 52 kDa Ro protein (Sjogren syndrome type A antigen) (SS-A) (Ro(SS-A))
 DB (Tripartite motif protein 21).
 GN SSM1 OR TRIM21 OR ROS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Macrophage;
 RX MEDLINE=96215393; PubMed=8625517;
 RA Kiech C.L., Gordon T.P., McCluskey J.;
 RT "Structural differences between the human and mouse 52-kD Ro
 RT autoantigens associated with poorly conserved autoantibody activity
 RT across species.";

RL Clin. Exp. Immunol. 104:255-263(1996).
 CC -1- FUNCTION: Ribonucleoprotein particle composed of a single
 CC polypeptide and one of four small RNA molecules. It is present in
 CC all mammalian cells studied but has no known function (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
 CC -1- SIMILARITY: Contains 1 SPRY domain.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: L27990; AB51154.1; -.
 DR MGD: MGI:106657; TrlM21.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR InterPro: IPR001870; B302.
 DR InterPro: IPR006574; PRY.
 DR InterPro: IPR003877; SPRY_receptor.
 DR InterPro: IPR000315; Znf_Box.
 DR InterPro: IPR01841; Znf_ring.
 DR Pfam: PF00622; SPRY; 1.
 DR Pfam: PF00643; zf-B_Box; 1.
 DR Pfam: PF00097; zf-C3H4; 1.
 DR PRINTS: PR01406; BBOXZNFINGER.
 DR SMART: SM00335; BBOX; 1.
 DR SMART: SM00589; PRY; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00449; SPRY; 1.
 DR PROSITE: PS00119; ZF_BOX; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Zinc-finger; Antigen; RNA-binding; Ribonucleoprotein; DNA-binding.
 FT ZN_RING 20 59
 FT ZN_RING 96 127 B BOX-TYPE.
 FT DOMAIN 215 236 LEUCINE-ZIPPER.
 FT SEQUENCE 470 AA: 54175 MW: 393AESAFA254855B CRC64;
 Query Match 21.1%; Score 528; DB 1; Length 470;
 Best Local Similarity 29.7%; Pred. No. 3.2e-24;
 Matches 146; Conservative 87; Mismatches 189; Indels 70; Gaps 18;

OY 7 DELGCTSLSTYODVSGCEHYFCRCITTEHWVQEOAGARDCECRRTFAEPALASL 66
 DB 16 EEVTCIPCLDPVEVSVSIECGHCFCEKISQ---VGKGGSGVCPVCRORFLKMLRPNR 71
 OY 67 KLANIVERYSFPLDAILNARRAAP--COAH-DKVKLFCLTDRLALCFCEDEPALHEOHV 123
 DB 72 HIANVNEVLKQI---AGNTKSTQETHCMHGEKLHLCFCEQDQALCWCAQSKRIHDH 127
 OY 124 QVTGIDDAFDELQRELKQALQALDSEHRETEALQ--LKROLAETKSTKSLRTTIGFAF 182
 DB 128 TRVPLEEAAQYQEKIHVLEKLRG--KELAEKEMDTMTQRTWKRIIDIOKSRTHAEF 186
 OY 183 ERLHRLEROKAMLEELADTARTLDIEOKVQRYSOGLKRYOGAGLIIOERLAETRH 242
 DB 187 ALQNSLQEOBORQRLQLEKQREYLRGKKE-----ALAEKQNALDELISELER- 238
 OY 243 TFLAGVASLSRLGK---IHTNLTYE-----DFTSKYTGCP-----LQY 280
 DB 239 -----RINGSELLEQVRIILERSGSNNLDTLIDADLDNSTCVPGRKKMLR 287
 OY 281 TTKMSLFQDHPVPAALTLDPGTAHQRLISDCTIVAYGNLHPROLQSPKRFDEVEVSV 340
 DB 288 TCM-----VH-----TLDNRTNWSMLISKDRQVMDPTH-QVNSDKERSNVPV 335
 OY 341 LGSFAFSSGVHWEEVVAEKTQWVIGLAHEAASRKSGIOIPSRGYCIAMHNGNOYSAC 400

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasai H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT *Functional annotation of a full-length mouse cDNA collection.*;
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Seems to play an important role in erythropoiesis.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
 CC -1- SIMILARITY: Contains 1 SPRY domain.
 CC -----
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 CC -----
 CC EMBL: AF14811; AAD28534.1; -
 CC EMBL: AF220121; AAG53494.1; -
 CC EMBL: AK011082; BAB27386.1; -
 CC MGD: MG1338757; Trm10.
 CC GO: GO:0005737; C:cytoplasm; IDA.
 CC GO: GO:0005515; F:protein binding activity; IPI.
 CC InterPro: IPR001870; B302.
 CC InterPro: IPR006574; PRY.
 CC InterPro: IPR003877; SPRY_receptor.
 CC InterPro: IPR000315; ZnF_Box.
 CC InterPro: IPR001841; ZnF_fing.
 CC Pfam: PF00643; zf-B_box; 1.
 CC Pfam: PF00097; zf-C3HC4; 1.
 CC SMART: SM00336; BBOX; 1.
 CC SMART: SM00589; PRY; 1.
 CC SMART: SM00184; RING; 1.
 CC SMART: SM00449; SPRY; 1.
 CC PROSITE: PS0119; ZF_BOX; 1.
 CC PROSITE: PS00518; ZF_RING_1; 1.
 CC PROSITE: PS0089; ZF_RING_2; 1.
 CC Zinc-finger; Coiled coil.
 CC ZN_FING 16 61
 CC ZN_FING 94 135
 CC DOMAIN 144 180
 CC DOMAIN 362 484
 CC CONFLICT 133 133
 CC CONFLICT 231 231
 CC CONFLICT 365 365
 CC CONFLICT 368 368
 CC SEQUENCE 489 AA; 55630 MW; AA7E26FABD120804 CRC64;
 Query Match 18.2%; Score 456; DB 1; Length 489;
 Best Local Similarity 28.0%; Pred. No. 5.8e-20;
 Matches 132; Conservative 84; Mismatches 222; Indels 34; Caps 12;

QY 227 EGAIILQERLAETDRHTFLAGVASLSERLKGKHEHNLVTEDEPTSTYTPLOY--TW 283
 Db 241 EKMKRFRAGLITLDRSLINCERFKRKPALISPQLRIQIRDFQAI--PLRQEMFTFL 298
 QY 284 KSLFQDHPNPAALITDPGRANORLLISDCTIVAYGNLHPQLQDSPKRDEVSVLGS 343
 Db 299 EKLCFELDYEPRAHSLDPTSHPLISEDHRRARF-SYKWNSPDTPORFDRVTVIAQ 357
 QY 344 EAFSSGVHYWEVVV--AEKTQWVIGLAHEAASRGSIQIOPSRGFCIVAHNGQVSACT 401
 Db 358 CGFTGGHHTWAVNDLHAGSCIVGVYREDYRRKRGELRLRPEGSIAMVRLAMGVSLG 417
 QY 402 EPTWRLNVRKLDKRVGVFLIDYDGLLIYFVADMSWLYTEREKKPGRLCSYF 453
 Db 418 FPLTRALBQPRVQVSLDYEGWITFVNAVQEHYFTFASPTQRIPLF 468
 RESULT 13
 RNF9_HUMAN
 ID RNF9_HUMAN STANDARD; PRT; 482 AA.
 AC Q9UDY6; 0960B6; 09C023; 09C024;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RING finger protein 9 (B30-RING finger protein) (Tripartite motif
 protein 10).
 GN TRIM10 OR RNF9 OR RFB30.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE-Testis;
 RX MEDLINE-97419168; PubMed-9271628;
 RA Henry J., Ribouchon M.-T., Depetris D., Mattel M.-G., Offer C.,
 RA Tazi-Ahni R., Pontarotti P.;
 RT *Cloning, structural analysis, and mapping of B30 and B7 multigenic
 RT families to the major histocompatibility complex (MHC) and other
 RT chromosomal regions.*;
 RL Immunogenetics 46:383-395(1997).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE-21231161; PubMed-11331580;
 RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Iuzi L.,
 RA Rigamelli D., Zanatta E., Messali S., Caimarca S., Guffanti A.,
 RA Minucci S., Pelicci P.G., Ballabio A.;
 RT "The tripartite motif family identifies cell compartments.*";
 RL EMBO J. 20:2140-2151(2001).
 RP [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RA Shima S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.*";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Seems to play an important role in erythropoiesis (by
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Name-Alpha;
 CC IsoId-Q9UDY6-1; Sequence-Displayed;
 CC Name-Beta;
 CC IsoId-Q9UDY6-2; Sequence-VSP_005748;
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- SIMILARITY: Contains 1 B box-type zinc finger.
 CC -1- SIMILARITY: Contains 1 SPRY domain.
 CC -----
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CC -----
DR EMBL: Y07829; CAB52384.1;
DR EMBL: AF220122; AAG53495.1;
DR EMBL: AF220123; AAG53496.1;
DR EMBL: AP000517; BAB63332.1;
DR Genew: HGNC:10072; TRIM10.
DR MIM: 605701;
DR GO: GO:0005622; C:intracellular; NAS.
DR GO: GO:0008270; F:zinc ion binding activity; NAS.
DR GO: GO:0030097; P:hemopoiesis; NAS.
DR InterPro: IPR001870; B302.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY_receptor.
DR InterPro: IPR000315; ZnF_Box.
DR InterPro: IPR001841; ZnF_finger.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; zf-B_Box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00589; PRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS00119; ZF_BOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Zinc-finger; Coiled coil; Alternative splicing.
DR ZN_FING 16 61
DR ZN_FING 94 136
DR ZN_FING 143 178
DR DOMAIN 363 482
DR VARSPLIC 370 482
VSIDLAGASCNVGVSEVORVKGLRLRREGVAVRIAM
GPNVSLGSPPTLTKEQPROVRSLSLSDVEGVATNATVR
EPITFTASFTKRVLPFGELMGSSFLSS -> WMAVVP
GDSGCQFCSPSVLGTVEVVA (in isoform beta).
/FTI-VSP_005748.
SR -> G (IN REF. 1).
SR -> E (IN REF. 3).
K -> E (IN REF. 1 AND 3).
S -> Y (IN REF. 2; AAG53496 AND 3).
A -> G (IN REF. 3).
SEQUENCE 482 AA; 55087 MW; 19354750602CD42C CRC64;
Query Match 18.0%; Score 449.5; DB 1; Length 482;
Best Local Similarity 27.5%; Pred. No. 14e-19;
Matches 132; Conservative 86; Mismatches 213; Indels 49; Gaps 14;
4 SLKDELCSICLSIYDVPVSLGCEHYFCRCITTEHW--VROBAQAGARCPCEGRRTFAEPA 61
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
9 SLADENVCPICOGTLREPVITDCGHNFCRACITRYCEIPGDLSESPICKEPRFGS 68
|||:||||:||||:||||:||||:||||:||||:||||:||||:
62 LAPSLAKLNIYERSSFPDLAIINARRARPCQAND--KVLFCITDRALLCFECDEPAL 119
|||:||||:||||:||||:||||:||||:||||:||||:||||:
69 FRPMWGLANVENETRLQVLSTLIGE-EDVQDEHSGSKRIYFECDEDEQQLCVCREAGE 127
|||:||||:||||:||||:||||:||||:||||:||||:||||:
120 HEQHCVTIDAFDELQELKDOALQDSEHREHVALQKKR---OLAEFTSSKSLRT 176
|||:||||:||||:||||:||||:||||:||||:||||:||||:
128 HATHTMRLEDAAPYRQIHKLCGLR-KEREQEELQSRKNKMQVLLTVGVSTK--RQ 184
|||:||||:||||:||||:||||:||||:||||:||||:||||:
177 TIGAEFRLHRLREROKAMELEADYARFLTDIQ-----KVQVYSOOLRVVQSGA 229
|||:||||:||||:||||:||||:||||:||||:||||:||||:
185 QVISEFAILRKFLERQOSILLAQLESQDGLRQNDERDVLVAGICFSAIIELEKN 244
|||:||||:||||:||||:||||:||||:||||:||||:||||:
230 QILDERLAETDRHFTL-----AGVASLSERLKGKIHETNLTLYEDPPTSKYTPPL 278
|||:||||:||||:||||:||||:||||:||||:||||:||||:
245 ERPARELLTDIRSTLIRCETRKCRKPVAVSPELGQRIR-----DFPQAL--PL 291
|||:||||:||||:||||:||||:||||:||||:||||:||||:
279 QYTI---KSLFQDIHPYPAALTDPGTAHQRLIISDCTIYAVGNLHPQLQDSPKRPD 335
|||:||||:||||:||||:||||:||||:||||:||||:||||:
292 QREKMKFLEKLCFELADEPRAHISDPTSHRKLISEDHORAFQSKM-QNSPDPRQRED 350
|||:||||:||||:||||:||||:||||:||||:||||:||||:
336 VEVSVLGESEAFSSGVHWEVYV--AEKTQWVIGLAHAASRGSQTQIDPSNGFYIVMHD 393
|||:||||:||||:||||:||||:||||:||||:||||:||||:

```

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DB 351 RATCVLAHTGTCGRFTWVVSIDLAGASCITGVGVEDVORRGELRLRPEGVAVRIAM 410
OY 394 GNOVSACEPTWRLNVRDLKDYGVFLDYDQGLIFLYNADDSMLTYTFREKPGKCSYF 453
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : |
DB 411 GFVSALGSFP-TRLTLKEQPROVRSLSLDEGVGVTFITNVTPEITFTASTKRVYIPFF 469

RESULT 14
ID 2173.HUMAN STANDARD; PRT; 539 AA.
AC 012899;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 173 (Tripartite motif-containing protein 26) (Acid
GN finger protein) (AFP).
GN TRIM26 OR ZNF173.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96079113; PubMed=8530076;
RA Chu T.W., Caposela A., Coleman R., Geel V.L., Nallur G., Gruen J.R.;
RT Cloning of a new 'finger' protein gene (ZNF173) within the class I
RT region of the human MHC.*;
RL genomics 29:229-239(1995).
RN 1;
RP SEQUENCE FROM N.A.
RA Shihna S., Tamliya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 H1A class I region.*;
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.*;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC 1- SIMILARITY: Contains 1 RING-type zinc finger.
CC 1- SIMILARITY: Contains 1 B box-type zinc finger.
CC 1- SIMILARITY: Contains 1 SPRY domain.
CC -----
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CC or send an email to licensel@sb-sib.ch).
CC -----
DB EMBL: 009825; AAA93131.1;
DR EMBL: AP000517; BAB63330.1;
DR EMBL: BC032297; AAH32297.1;
DR Genew: HGNC:12962; TRIM26.

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MIM: 600830: -
 DR GO: 0003677: F:DNA binding activity; TAS.
 DR GO: 0005515: F:protein binding activity; TAS.
 DR InterPro: IPR001870; B302.
 DR InterPro: IPR006574; PRY.
 DR InterPro: IPR003877; SPRY_receptor.
 DR InterPro: IPR000315; Znf_Box.
 DR InterPro: IPR001841; Znf_Fing.
 DR Pfam: PF00642; SPRY.1.
 DR Pfam: PF00643; zf-B_box.1.
 DR Pfam: PF00097; zf-C3HC4.1.
 DR PRINTS: PR01406; BBOXZNFINGER.
 DR SMART: SM00336; BBOX.1.
 DR SMART: SM00589; PRY.1.
 DR SMART: SM00184; RING.1.
 DR SMART: SM00449; SPRY.1.
 DR PROSITE: PS00119; ZF_BOX.1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS00089; ZF_RING_2; 1.
 DR Zinc-finger: Coiled coil.
 KW Zinc-finger; Coiled coil.
 FT ZN_FING 16 57 RING-TYPE.
 FT ZN_FING 97 138 B_BOX-TYPE.
 FT DOMAIN 188 227 COILED COIL (POTENTIAL).
 FT DOMAIN 365 539 SPRY.
 FT DOMAIN 388 400 POLY-GLU.
 FT DOMAIN 422 432 POLY-GLU.
 SQ SEQUENCE 539 AA: 62165 MW: 842A71C41F2E2348 CRC64;

Query Match 17.9%; Score 449; DB 1; Length 539;
 Best Local Similarity 24.9%; Pred. No. 1,7e-19;

Matches 15; Conservative 96; Mismatches 192; Indels 120; Gaps 16;

4 SIKDELICISLIVDPVSLGCHYFCRCRTEHNVROEAGADCEPCRRTPAPALA 63
 9 SLEEVYTCISICLDYLDPTVITDGHVFCRSCSTD--VRPISGSRVPCPLCKKFKENIR 66
 64 PSIKLANIYERYSFPLD-----ALNARRARPCQAH-DKATKCLIDRALLCFPCDE 116
 67 PWQGLASLVENIERKLVNDGRGROGEYTRQODAKLERHEKHYCCEDGKLLCYWCRE 126
 117 PALHEQHYTGIDDAFDELORELKDLQALDSEERHTEALQILKRLAETKSTSL-- 174
 127 SREHRHTAVIMEKAQPHREKTLNHLSTLR-RDRKIKIGFO--ANGADILAAKRLQD 183
 175 -RTTIGEAERLRLIREKOKAMLELE-----ADTARTLTDE 212
 184 QKQYIAAEFEQGHQFLEREHLLQJLAKLEQELTEGREKFKSGYGEIARLALVISELE 243
 213 QVQVRSQLRKVQEGAOILQER--LAETDRITFLAG--VASLSERLKGKIHETMLTYE 267
 244 GRAQ-----QPAELMODRDLNRPYPRKRFVWGRPIARVAVKKTGCEFSDKLLSIQ 294
 268 DEPTSKYTPGLQYTIKSLFODIHVPALITLDPGTAHRLIISDCTIYAVGNLHPPL 327
 295 R-GLRERFG-----KILRDEIKTVSVTLDPQASGTLQISEMKCYTYSLYKSAY 345
 328 QDSKPRFDEVSLGSEAFSGVYWEVVAEKTQ----- 363
 346 L-HPOGFDEPGVIGSKFTWGVYWEV-EREKGSDEBEGDEBEGDEBEGDEBEGAGY 403
 364 -----VGLAHEAASRKGSIQIOPSRGYCT 369
 404 GQCYDMETDEDEESLGDEEBEEBEEBEEBEEBEEBEEBEEBEEBEEBEEBEEBEEB 463
 390 VNHIDNQYSACTEPTRLNVRDKLVGVFLVDYDGLLFYVNDADMSMLYTFEKEPGRK 449
 464 RLSSSGITW-ANTSPKELPALPRRVGALDTEGGTFTVNAESELITTFATPTTRL 522
 450 CSY 452
 523 VPF 525

RESULT 15
 ID TM15_HUMAN STANDARD; PRT; 465 AA.
 AC O9C019; O95604; O9C018;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tripartite motif protein 15 (Zinc finger protein B7).
 GN TRIM15 OR ZNF87.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1 AND 2), AND VARIANT VAL-29.
 RX MEDLINE-21231161; PubMed-11331580;
 RA Raymond A., Meroni G., Fantozzi A., Meila G., Cairo S., Iuzi L.,
 RA Riganeil D., Zanaria E., Messali P.G., Ballabio A.,
 RA Minucci S., Pellici P.G., Ballabio A.;
 RT "The tripartite motif family identifies cell compartments";
 RL EMBO J. 20:2140-2151(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT VAL-29.
 RA Goel V.L., Kuida S., Chu T.W., Bowles C., Gruen J.R.;
 RT "A cluster of genes proximal to HLA-A encode putative zinc finger
 RT proteins";
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Shihina S., Tamaiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Name-1: Synonyms=Alpha;
 CC Name-2: Synonyms=beta;
 CC Name-3: Synonyms=gamma;
 CC Name-4: Synonyms=delta;
 CC Name-5: Synonyms=epsilon;
 CC Name-6: Synonyms=zeta;
 CC Name-7: Synonyms=eta;
 CC Name-8: Synonyms=theta;
 CC Name-9: Synonyms=iota;
 CC Name-10: Synonyms=kappa;
 CC Name-11: Synonyms=lamda;
 CC Name-12: Synonyms=muetra;
 CC Name-13: Synonyms=nun;
 CC Name-14: Synonyms=xi;
 CC Name-15: Synonyms=omicron;
 CC Name-16: Synonyms=pie;
 CC Name-17: Synonyms=rho;
 CC Name-18: Synonyms=sigma;
 CC Name-19: Synonyms=tan;
 CC Name-20: Synonyms=upsilon;
 CC Name-21: Synonyms=phi;
 CC Name-22: Synonyms=chi;
 CC Name-23: Synonyms=psi;
 CC Name-24: Synonyms=omega;
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 CC Name-99: Synonyms=unbecomingly;
 CC Name-100: Synonyms=unseemingly;

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OM protein - protein search, using sw model

Run on: October 7, 2003, 17:46:56 ; Search time 30 Seconds
(without alignments)
669,922 Million cell updates/sec

Title: US-09-927-091-1
Perfect score: 2504
Sequence: 1 MACSLDELICISICISYOD.....GOSHANGKNVQPLRINTVRI 4/75

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/1aa/5a_COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5b_COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6a_COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6b_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546.5	21.8	487	2	US-08-724-394A-7
2	486	19.4	485	2	US-08-724-394A-8
3	364.5	14.6	413	4	US-09-663-600A-198
4	321	12.8	610	2	US-08-724-394A-5
5	305.5	12.2	540	2	US-08-724-394A-4
6	299	11.9	581	2	US-08-724-394A-2
7	295.5	11.8	581	2	US-08-724-394A-3
8	275.5	11.0	589	2	US-08-724-394A-1
9	248.5	9.9	353	4	US-09-484-970B-171
10	181	7.2	158	4	US-09-663-600A-104
11	168.5	6.7	100	4	US-09-230-196-5
12	166.5	6.6	588	5	PCT-US93-05794-3
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14	144.5	5.8	209	4	US-09-461-325-468
15	144.5	5.8	435	4	US-09-561-989-10
16	137.5	5.5	658	1	US-08-190-802A-34
17	137.5	5.5	658	1	US-08-477-346-34
18	137.5	5.5	658	4	US-08-473-089-34
19	137.5	5.5	658	4	US-08-487-072A-34
20	134.5	5.4	47	2	US-08-691-814B-20
21	133.5	5.3	450	2	US-08-818-514-6
22	133.5	5.3	450	3	US-09-115-934A-6
23	133.5	5.3	450	4	US-09-611-175-6
24	133.5	5.3	560	2	US-08-095-728B-6
25	133.5	5.3	560	5	PCT-US92-02320A-6
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27	133.5	5.3	797	5	PCT-US92-02320A-2

28	133	5.3	312	1	US-08-425-061-18	Sequence 18, Appl
29	133	5.3	312	2	US-08-825-886-18	Sequence 18, Appl
30	133	5.3	312	4	US-08-989-890-18	Sequence 18, Appl
31	133	5.3	765	1	US-08-425-061-19	Sequence 19, Appl
32	133	5.3	765	2	US-08-825-886-19	Sequence 19, Appl
33	133	5.3	765	4	US-08-989-890-19	Sequence 19, Appl
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35	133	5.3	900	2	US-08-825-886-20	Sequence 20, Appl
36	133	5.3	900	4	US-08-989-890-20	Sequence 20, Appl
37	133	5.3	914	1	US-08-425-061-21	Sequence 21, Appl
38	133	5.3	914	2	US-08-825-886-21	Sequence 21, Appl
39	133	5.3	914	4	US-08-989-890-21	Sequence 21, Appl
40	133	5.3	1202	1	US-08-425-061-22	Sequence 22, Appl
41	133	5.3	1202	2	US-08-825-886-22	Sequence 22, Appl
42	133	5.3	1202	4	US-08-989-890-22	Sequence 22, Appl
43	133	5.3	1363	1	US-08-425-061-23	Sequence 23, Appl
44	133	5.3	1363	2	US-08-825-886-23	Sequence 23, Appl
45	133	5.3	1363	4	US-08-989-890-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-724-394A-7
Sequence 7, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Laufer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolf, Roger K.
TITLE OF INVENTION: Megadase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..487
OTHER INFORMATION: /note= *52 kd Ro*
US-08-724-394A-7


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; PRIOR APPLICATION NUMBER: 60/069, 957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074, 121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081, 563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096, 116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099, 273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO: 198
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37..-1
US-09-663-600A-198

```

Query Match 14.6%; Score 364.5; DB 4; Length 413;

Best Local Similarity 26.4%; Pred. No. 5, 1e-26;

Matches 115; Conservative 79; Mismatches 170; Indels 71; Gaps 15;

```

QY 4 SIKDELCSICSTIYQDPVSLGCEHYFCRCITTEHWRODA----GANDCPECRTFAE 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 NVOEETVCICIELTEPLESLDCGHSICRACITVS--NKEAVTSMGKSSCPVCISYSF 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 PALAPSLKANTVERSSFPDLAINARBARPCQAH-DKVTLCFLTDALLCFEDDEA 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 66 EHLQANQHLANTIVERLKEVKLSPDNGKKDL--CDHNGEKLLFECKEDRKVICWLERSQ 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 LHEHQVGTGIDAFDELQRELKDLOALQDSEREHTEALQLKROLAETKSSPK---SL 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 EHRGHTVTLTEVFEKCGCKLAVALKRLKEEEE---AKLEADIREKTSKKYVOTE 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 RTTIGAEFRHLRLEROKAMLELEADTARTLDIEQVORYSOQLKRVDE----- 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 180 RORIQEFQDLRSILNNEQREQLREBEKKTLDFAEADELVQOKOLVRELISDVGC 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 -----GAOILQRLAETDHTFLGAVASIE--RLKGRHENTLTYEDPTSKYTPLOY 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 240 RQWSTWMLDQ-----MSGIMKWSLWRLK---KPKMSKKLKTFFHADLSR 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 TTKMSLFQDHPVP---AALTLDPGTAHQRLILSDCTIYVAGNLHPQPLQDSPKRFVE 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 286 ML--QMFRELPAVRQWVDVTLNSVNLNLVLSEDRQVIVSPIRPGCYN----- 335
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 VAVLSSEAFSSGVHYWEVVAEKTQVIG-----LAHEAASRKG-SIQIQPSR 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 336 YGVLSQYFSSGKHWEVDVSKRTAWILGVYCRITYSRHMKYVVRRCANQNILYTKRPLF 395
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 385 GFYCIYMHGNOYSA 399
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 396 GTWVIGLQNKCKTGA 410
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 4

US-08-724-394A-5

Sequence 5, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Kronmal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies thereo

NUMBER OF SEQUENCES: 31

NUMBER OF SEQUENCES: 31

```

; CORRESPONDENCE ADDRESS:
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; City: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-Oct-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..610
; OTHER INFORMATION: /note="BTF3"
US-08-724-394A-5

```

Query Match 12.8%; Score 321; DB 2; Length 610;

Best Local Similarity 34.7%; Pred. No. 1, 3e-21;

Matches 82; Conservative 45; Mismatches 87; Indels 22; Gaps 8;

```

QY 218 YSQQLKRVQGAQILDER-----LAETDRH-FLAGVASTSLRCKIHERMLTYEDRP 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 287 WRQCKEKIALSRTEREREKREKMGVATQELISXXXXXXLRKLEDEELKWRRIQ---- 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 TSKYTPLOYTTIK-SLFQDHPVPAALTLDPGTAHQRLILSDCTIYVAGNLHPQ--- 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 343 MARGESIAVHEKMAKLFK-----PADVILDPRTANAILLVSDQSVQRAE-EPDXXX 396
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 LQDSPKRFDEVSYLSEAFSSGVHYWEVVAEKTQVIGLAHEAASR-KGSIQIQPSRG 385
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 397 LPDNPFRFWRKYCVLCCENFTSGRHWEVEVCDRKEMHIGVCSKNVERKKGWKMPENG 456
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 386 FVCIYVMDHNOVSACIEPWTRLNVRDKLDKVGVFLLYDGLLIFYAADMSTLYTF 441
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 457 YWTGILDGKRYALTEPRINLKLPPRPKVGIFLDYETGEISFYATGSHLYTF 512
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 5

US-08-724-394A-4

Sequence 4, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Kronmal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies thereo

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

```

1 ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
2 STREET: Two Embarcadero Center, 8th Floor
3 CITY: San Francisco
4 STATE: CA
5 COUNTRY: USA
6 ZIP: 94111-3834
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patent In Release #1.0, Version #1.30
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/724,394A
16 FILING DATE: 01-OCT-1996
17 CLASSIFICATION: 536
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Pitts, Renee A.
20 REGISTRATION NUMBER: 35,136
21 REFERENCE/DOCKET NUMBER: 017957-000100
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 415-576-0200
24 TELEFAX: 415-576-0300
25 INFORMATION FOR SEQ ID NO: 4:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 540 amino acids
28 TYPE: amino acid
29 STRANDEDNESS: not relevant
30 TOPOLOGY: not relevant
31 MOLECULE TYPE: peptide
32 FEATURE:
33 NAME/KEY: Region
34 LOCATION: 1-540
35 OTHER INFORMATION: /note="BTF5"
36
37 US-08-724-394A-4
38
39 Query Match 12.2%; Score 305.5; DB 2; Length 540;
40 Best Local Similarity 42.5%; Pred. NO. 3e-20;
41 Matches 71; Conservative 28; Mismatches 57; Indels 11; Gaps 5
42
43 QY 280 YTIW-KSLFQIHPPALTLDPGTAHQRLIISDCTIVANGNLHPQ---LQDSPKRPD 335
44 352 YENKRAKLFK----PADVILDPKTPANPILLYSEDSORVORAK-EPQDXXKLPDPNPERFN 405
45
46 QY 336 VEVSVLSEAFSSGVHYWEVVAEKTQWVIGLAHBAASRK-GSIOIOPSRGFYIVMDG 394
47 406 WHYCVLGEESTISGRHYWEVEYGRKKEHIGVCSKNVQRKKGWAMTFENGFWTGLTDG 465
48
49 QY 395 NOYACACEPWTRLNVRKLDKRVGVFLDYDQGLLIFYNADNDSWLYTF 441
50 466 NKRYTLLEPRTNLKLPPKPKRVGVFLDYETGDISFYNAVDSSHHTF 512
51
52 RESULT 6
53 US-08-724-394A-2
54 Sequence 2, Application US/08724394A
55 Patent No. 5872237
56
57 GENERAL INFORMATION:
58 APPLICANT: Feder, John N.
59 APPLICANT: Krommal, Gregory S.
60 APPLICANT: Lauer, Peter M.
61 APPLICANT: Ruddy, David A.
62 APPLICANT: Thomas, Winston
63 APPLICANT: Tsuchihashi, Zenta
64 APPLICANT: Wolff, Roger K.
65 TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
66 TITLE OF INVENTION: Sequences and Antibodies Thereof
67 NUMBER OF SEQUENCES: 31
68 CORRESPONDENCE ADDRESSES:
69 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
70 STREET: Two Embarcadero Center, 8th Floor
71 CITY: San Francisco
72 STATE: CA
73 COUNTRY: USA

```

```

ZIP: 94111-3634
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fils, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..581
OTHER INFORMATION: /note="BTF1"
US-08-724-394A-2

Query Match          11.9%; Score 299; DB 2; Length 581;
Best Local Similarity 37.3%; Pred. No. 1,4e-19;
Matches 72; Conservative 26; Mismatches 63; Indels 32; Gaps 6;

QY      297 LTLDPGTAHQRLILSD-----CIYVYGNLHPQLADSPKRFPEVEVSIGSEAFSSGV 350
       : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      365 VLLDPRDAHNPDLFSEDGRSVRCFCFRILGESVP-----DNPERFSQCVCYLGRESFASGK 420
QY      351 HYWEVVAAEKTQWYIYGLAEHSAKR-GSIQIQPSRGFYCIYMHGDNOYSACTEPTRLNV 409
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      421 HYWEVEVENVTIEWTVGCDSVERKKGVLLIPONGFWTLEMHXKGQYRAVSSPRTIPL 480
QY      410 RDKLDKGVFLDYDOGILLIFYNADMSLYT-----PR-----EKFPKILSY 452
       : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      481 KESLCRAGVFIDYEAGDVSYTNMDRSHTYCPSASFSVPVFFPRLCKEDSPLITC-- 538
QY      453 FSPGOSHANGKNV 465
       : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      539 --PALTGANGTYV 549

RESULT 7
US-08-724-394A-3
; Sequence 3, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Rudd, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3634

```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01/957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..581
OTHER INFORMATION: /note="BTF2"
US-08-724-394A-3

Query Match
Best Local Similarity 42.3%; Pred. No. 3e-19; DB 2; Length 581;
Matches 63; Conservative 24; Mismatches 59; Indels 3; Gaps 2;

QY 295 AALTDPTGAHRLISDCTIVAYGNLHPQ--PLQDSPKRPDEVSVLGSSEAFSSGVHY 352
DB 363 ADVLDPTGAHRLFLSEDRSRVGRPYQKXXVDPNDRERDSQCVLGWESFASGRHY 422
QY 353 WEVVAEKTQWYIGLAHEAASRK-GSIQIQSRGFYCIYMDGNQYSACTEPMTLNVDRKL 411
DB 423 WEVEVENWVMTGVCGRHSVERKXGEVLLIPONGFMTLEMFNGNOYRALSPERILPLKE 482
QY 412 KLDKGVFLDYDOGLLIIFYNADMSWLYT 440
DB 483 SICRGVFLDYRAGDVSYFNMDRSHIYT 511

RESULT 8
US-08-724-394A-1
Sequence 1, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Laufer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
```

```
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01/957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..589
OTHER INFORMATION: /note="BT"
US-08-724-394A-1

Query Match
Best Local Similarity 11.0%; Score 275.5; DB 2; Length 589;
Matches 70; Conservative 25; Mismatches 74; Indels 9; Gaps 5;

QY 297 LTLDPTGAHRLISDCTIVAYGNLHPQ--PLQDSPKRPDEVSVLGSSEAFSSGVHY 354
DB 363 VTLDPPTAHPFLFLEDSKSVRLSDSRQKXXLPETERFDSWPCVLAGRETFSGRHYE 422
QY 355 VVAEKTQWYIGLAHEAASRK-GSIQIQSRGFYCIYMDGNQYSACTEPMTLNVDRKL 413
DB 423 VEVGDRIDALIGCRNNVAKKXGFDPTENGFMATLXGNGYALTLTRPPLAGRP 482
QY 414 DKVGVFLDYDOGLLIIFYNADMSWLYTFRP-KPFGKLCYFSPGOSHANGKNOPLRI 470
DB 483 RRVGIFLDYESGDISFNNMDSDIYTFGNVTFSGPLRFFFCIMSS---GK-KPLTI 535

RESULT 9
US-09-484-970B-171
Sequence 171, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmutz, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 171
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. 6426186 3575519CD1 (GENE ID 247384)
US-09-484-970B-171

Query Match
Best Local Similarity 9.9%; Score 248.5; DB 4; Length 353;
Matches 83; Conservative 66; Mismatches 129; Indels 55; Gaps 15;

QY 4 SIKDELCSICISYODP-VSLGCEHYFCRCITE-----HWVROEAQ-----GARDC 50
DB 16 NLEKOLICPICLEMFKPVYILPCQCNLCRKACANDIFOQANPYWTSGSSVSMGGRFC 75
QY 51 PECKRTFAEP-----ALAPSLKIANIVERY-----SSPFDALIANARRARP-CQAH--DK 98
```

```

Db      76 PTCHEVIMDRHGVYGLQRLNLYENITDIYKQECSSRPL-----QKGSHPMCKEHDEK 129
      99 VKLECLDRALLCFCEDEPALHEQHYTGIDDAFDELOREIKDQLAL-ODSEHEFEAL 157
      130 INIYCLCEPPTGCMKCVFGRHACCEVAPLOSVOGQKTELNINISMLVAGNDVOTIIT 189
QY      158 QLKROLAEKSSKSTKSTRTTIGAFERHLRLRERQKAMELEADYARTLTIDIEQVQR 217
      190 Q-LEDSRYVTKENSHQVEELSKQFTDLVAILDEKSELLQRTIQEOKELSFYEALIQ 248
QY      218 YSOOLRVQGAQIOLRIAEETDRHTPLAG----VASLSEKLG-KIHENLTVE--DFP 270
      249 YQEDLDSTKLVEYTAISLDEPGATFLTRAKOLIKSIVASKCQQLKTEQGEENDF- 307
Db      271 TSKYTGPLYTIWKSLEFQDIHPVPAALTDPGT 303
      308 ---FTLDLE-----HIALALRAIDPGT 326

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RESULT 10
US-09-663-600A-104
: Sequence 104, Application US/09663600A
: Patent No. 6573068
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, Jean-Baptiste
: APPLICANT: Duclet, Aymeric
: APPLICANT: Bougueleret, Lydie
: TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
: FILE REFERENCE: 31-US3.CIP
: CURRENT APPLICATION NUMBER: US/09/663,600A
: CURRENT FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: 09/191,997
: PRIOR FILING DATE: 1998-11-13
: PRIOR APPLICATION NUMBER: 60/066,677
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/069,957
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/074,121
: PRIOR FILING DATE: 1998-02-09
: PRIOR APPLICATION NUMBER: 60/081,563
: PRIOR FILING DATE: 1998-04-13
: PRIOR APPLICATION NUMBER: 60/096,116
: PRIOR FILING DATE: 1998-08-10
: PRIOR APPLICATION NUMBER: 60/099,273
: PRIOR FILING DATE: 1998-09-04
: NUMBER OF SEQ ID NOS: 229
: SOFTWARE: Patent.pm
: SEQ ID NO 104
: LENGTH: 158
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SIGNAL
: LOCATION: -37..-1
US-09-663-600A-104

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Query Match 7.2%; Score 181; DB 4; Length 158;

Best Local Similarity 34.1%; Pred. No. 2,7e-09;

Matches 44; Conservative 20; Mismatches 55; Indels 10; Gaps 5;

```

QY      4 SLKDELCSICLSIYQDPVSLGCEHYFCRCITIEHWYRQA-----QCARDCPECRRTFAE 59
      8 NVOEYVCPICLETLEPLSLDCGHSICRACITVS--NKEAVTSMGKSSCPVCGISYSF 65
Db      60 PALAPSLKLANIYERSSFPDLAILNRRARPCQAH-DKVKLFCLDRALLCFCEDEPA 118
      66 EHLQANQHRANIYERLKEVKLSPDNGKKRL--CDHNGEKLILFCKEDRVKICWLCSRSQ 133
QY      119 LHEQHQVTG 127
      124 EHRGHH-TG 131

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```

RESULT 11
US-09-230-196-5
: Sequence 5, Application US/09230196
: Patent No. 6307035
: GENERAL INFORMATION:
: APPLICANT: Rauscher III, Frank J.
: APPLICANT: Jensen, David E.
: TITLE OF INVENTION: BRCA1 Associated Protein (BAP-1) and
: TITLE OF INVENTION: Uses Therefor
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Howson and Howson
: STREET: Spring House Corporate Cntr., PO Box 457
: CITY: Spring House
: STATE: Pennsylvania
: COUNTRY: U.S.A.
: ZIP: 19477
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/230,196
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/022,997
: FILING DATE: 02-AUG-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/038,109
: FILING DATE: 19-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Bak, Mary E.
: REGISTRATION NUMBER: 31,215
: REFERENCE/DOCKET NUMBER: WST68BUSA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-540-9200
: TELEFAX: 215-540-5818
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 100 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
US-09-230-196-5

Query Match 6.7%; Score 168.5; DB 4; Length 100;
Best Local Similarity 37.6%; Pred. No. 2e-08;
Matches 35; Conservative 15; Mismatches 40; Indels 3; Gaps 2;

QY      5 LKDELCSICLSIYQDPVSLGCEHYFCRCITIEHW-VROAAGARDCPECRRTFAEPALA 63
      9 IKREVCPICLETLEKKEVSADCNHSFCRACITLTNYESNRNTDCKNGKPCVGRVYPGNGR 68
Db      64 PSKLANIYERSSFPDLAILNRRARPCQAH 96
      69 PNLHVANIYERLAGF--KSIPEERQKYNICQAH 99

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RESULT 12
US-07-903-466-3
: Sequence 3, Application US/07903466
: Patent No. 5395767
: GENERAL INFORMATION:
: APPLICANT: Murmane, John P.
: APPLICANT: Painter, Robert B.
: APPLICANT: Kapp, Leon N.
: APPLICANT: Yu, Loh C.
: TITLE OF INVENTION: Gene for Ataxia-telangiectasia
: TITLE OF INVENTION: Complementatation Group D (ATDC)

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NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
CITY: San Francisco
STATE: California
COUNTRY: San Francisco
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,466
FILING DATE: 19920622
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-077-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9275
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-07-903-466-3

Query Match
Best Local Similarity 26.6%; Score 166.5; DB 1; Length 588;
Matches 62; Conservative 36; Mismatches 92; Indels 43; Gaps 11;

QY 25 GCENHFCRCITENHWROGACRDCPECRRTFAEPALAPSCLKA-----NIVERYSSPP 79
DB 167 GSEEVLCDSICGN--KORA--VKSCLVQASFCFELHLPHEGAFRDHQLLEPIRDF- 220
QY 80 LDAIINARARPCQANDK-VKLFCLTDALCLCFPC--DEPALHEHOYTGIDDADEQ 136
DB 221 -----EARKCPHGKTMELFCOTDTCICICLMFOE---HNKHSVTVEEAKAEKE 268
QY 137 RELKQQLQALDSEERHTEALQILKRLAETKSTKSLRTTIGAEFERLRL--REKQ 193
DB 269 TELSLQKQQLQKIIEDEAEKWKQEKRIKSFITNEKAILLEQNFRDLVRLDKQKEV 328
QY 194 KAMLELE---ADTATLTLDI-----EOKVQYRSQLKRVQEGAOIQE 234
DB 329 RAALRQEDAVQKVIQMDALDERAKVLEHDKQTR--EQLHSISDSVLEQ 379

RESULT 13
PCT-US93-05794-3
Sequence 3, Application PC/TUS9305794
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Gene for Ataxia-telangiectasia
TITLE OF INVENTION: Complementatation Group D (ATDC)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Leona L. Lauder
STREET: 177 Post Street, Suite 800
CITY: San Francisco
STATE: California
COUNTRY: San Francisco
ZIP: 94108-4731
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05794
FILING DATE: 19930618
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,466
FILING DATE: 22-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-077-1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-421-4973
TELEFAX: 415-421-1663
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
PCT-US93-05794-3

Query Match
Best Local Similarity 26.6%; Score 166.5; DB 5; Length 588;
Matches 62; Conservative 36; Mismatches 92; Indels 43; Gaps 11;

QY 25 GCENHFCRCITENHWROGACRDCPECRRTFAEPALAPSCLKA-----NIVERYSSPP 79
DB 167 GSEEVLCDSICGN--KORA--VKSCLVQASFCFELHLPHEGAFRDHQLLEPIRDF- 220
QY 80 LDAIINARARPCQANDK-VKLFCLTDALCLCFPC--DEPALHEHOYTGIDDADEQ 136
DB 221 -----EARKCPHGKTMELFCOTDTCICICLMFOE---HNKHSVTVEEAKAEKE 268
QY 137 RELKQQLQALDSEERHTEALQILKRLAETKSTKSLRTTIGAEFERLRL--REKQ 193
DB 269 TELSLQKQQLQKIIEDEAEKWKQEKRIKSFITNEKAILLEQNFRDLVRLDKQKEV 328
QY 194 KAMLELE---ADTATLTLDI-----EOKVQYRSQLKRVQEGAOIQE 234
DB 329 RAALRQEDAVQKVIQMDALDERAKVLEHDKQTR--EQLHSISDSVLEQ 379

RESULT 14
US-09-461-325-468
Sequence 468, Application US/09461325A
Patent No. 6475753
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,509
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,510
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 468
LENGTH: 209

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TYPE: PRT
ORGANISM: Homo sapiens
US-09-461-325-468

Query Match 5.8%; Score 144.5; DB 4; Length 209;
Best Local Similarity 29.1%; Pred. No. 1.2e-05;
Matches 46; Conservative 23; Mismatches 84; Indels 5; Gaps 2;

QY 299 LDPGTAHQRLISDCTIVAG--NLHPQLQDSPKREDVEVSVLGSEAFSSGVHWEVY 356
DB 37 LEETAISSIALFRDDGVKGLVGLPTKALNVERFERNAVYLAOTATSGRHWEVY 96
QY 357 VAETQWYVIGLAHFAASRKSIOIQPSRGYCIYHMDGNOYSACTEPWTRLNVRDKLDKY 416
DB 97 VKRSQGFRIQVADVDMRSDSCIGVDDRSWFTMPASAGTQPCWPTKPOLRVL--GSOEV 153
QY 417 GVFIDYDQGLIFYNADMSWLYTFREKPGKLCYSFS 454
DB 154 GLLEYEQKLSLVDSQSVVHTLQTFDGRVYPAFA 191

RESULT 15

US-09-561-989-10
Sequence 10, Application US/09561989
Patent No. 6468750
GENERAL INFORMATION:
APPLICANT: KOLLER, Klaus-Peter
TITLE OF INVENTION: No. 6468750el Cell Regulation Factor T1020
FILE REFERENCE: aeq
CURRENT APPLICATION NUMBER: US/09/561,989
CURRENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 435
TYPE: PRT
ORGANISM: Homo sapiens
US-09-561-989-10

Query Match 5.8%; Score 144.5; DB 4; Length 435;
Best Local Similarity 19.0%; Pred. No. 3.8e-05;
Matches 81; Conservative 69; Mismatches 178; Indels 99; Gaps 15;

QY 1 MACSLKDE-----LICSICLSITYQDPVSLCEHYFCRCITTEHMYROEAOGARDCEPCR 54
DB 51 LKCOLCEKAPKEATVYMCQCVFYCDPCRLRC--HPRGRPLAKHRLVPPAOG----- 100
QY 55 RTFAEPALAPLKLANIYERYSFPLDALNARRARPCQAH--DKVLFCTDRALICF 112
DB 101 -----RVSRRISP-----RKVSTCTDHELENHSMTCVOCCKMPYCY 135
QY 113 FCDEPALHEQHVGTGIDAFDELQRELKQLOALQDSEREHTALQLKROLAETKSSTK 172
DB 136 QCLEGKSHSHVAKLGMWKLHKSQSLQALNGLSBRAKEAKFVLQLRNVVQOIQENS 195
QY 173 SLRTTIGAEFERLHLREKAKMLELEADTARTLDEQVQKYSQGLKRVQEGAIL 232
DB 196 EFACLVACDAILDALRRKAKLARYNKEHKLKVVARDQISHCTVAKRLQGTGLMEYC 255
QY 223 QERLAETDRHTEFLAGVASLSRLKGIHET-----NLJ---YEDPFTSKYTGPIQYTI 282
DB 256 LEVIKENDPSGFL-----QISDALIRVHLETDQMGKGLTPRMVTDPLSLDNSPLQSI 311
QY 283 WKSLEFQDI--HPVPAALITDPGTAHQRLISDCTIVAGNLHPQLQDSPKREDVEVS 339
DB 312 HOLDFVQVYKASSPVATPIQ-----LEBECT--HNNSATLSWKOPP-----LS 353
QY 340 VLGSFAF-----SSGVYWEYVVAEKTQWYIGLAH-----EASRKG-----SI 378
DB 354 TVPADGYTLELDGNGGOFREYVYKETMCTVDGLHFNSTYNARYKAPNKTGVSPSKTL 413
QY 379 QIOPSRG 385
:| | |

DB 414 VIOTSEG 420

Search completed: October 7, 2003, 17:52:00
Job time : 32 secs